

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 2, 2004, 16:20:22 / Search time 17 Seconds

(without alignments)  
1997.389 Million cell updates/sec

Title: US-10-017-390A-397

Perfect score: 1828  
Sequence: 1 MPWPLLLLVASGQTRPC.....KVPILHCVDTRSNARGPILL 353

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 500 summaries

Database:

1: PIR 78:\*  
2: PIR1:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1235	67.6	242	2	T14791
2	279.5	15.3	662	2	S42799
3	265	14.5	907	2	JE0176
4	263	14.4	707	2	UC0763
5	257	14.1	907	2	UC0193
6	247	13.5	560	2	A60164
7	236.5	12.9	312	1	NBRH29
8	234.5	12.6	605	2	UC5239
9	230.5	12.6	1091	2	A58532
10	225	12.3	1531	2	T42218
11	224.5	12.3	605	2	A41915
12	217	11.9	738	2	T19398
13	215.5	11.8	603	2	UC1282
14	215.5	11.8	1066	2	T15854
15	215	11.8	1389	2	T13852
16	214.5	11.7	603	2	UC6188
17	213	11.6	1385	2	T13887
18	212	11.6	357	2	S24317
19	211.5	11.6	1256	2	S60461
20	210.5	11.5	1523	2	T13953
21	210	11.5	836	2	T46070
22	206	11.3	622	2	UC7973
23	203	11.1	458	2	T19941
24	203	11.1	575	2	T29972
25	201.5	11.0	526	2	C84552
26	201.5	11.0	680	2	T19939
27	201	11.0	961	2	T23395
28	199	10.9	1119	2	AD1822
29	198	10.8	354	2	S29145

30	197	10.8	536	2	A34901	lysine carboxypept
31	197	10.8	1134	1	A29944	chaoprin precursor
32	195.5	10.7	360	2	S06280	decorin precursor
33	195.5	10.7	360	2	T47020	decorin - rabbit
34	194.5	10.6	354	2	A55454	decorin precursor
35	194	10.6	1051	2	T13174	gpi50 protein - fr
36	193.5	10.6	342	2	A46743	lumican precursor
37	192	10.6	1778	2	AF1116	internalin protein
38	190.5	10.4	359	1	NBRH08	decorin precursor
39	189.5	10.4	369	2	S32559	biglycan precursor
40	183.5	10.0	338	2	S52284	lumican, secretory
41	183.5	10.0	369	2	S20811	proteoglycan I - m
42	183.5	10.0	369	2	S32793	biglycan precursor
43	183.5	10.0	424	2	S27793	hypothetical prote
44	181.5	9.9	343	2	A41748	lumican precursor
45	181.5	9.9	1257	2	A68536	protein B0523.5 [i
46	181	9.9	496	2	C96832	hypothetical prote
47	181	9.9	789	2	T28714	hypothetical prote
48	181	9.9	1355	2	T28715	hypothetical prote
49	180.5	9.9	440	2	A47530	oligodendrocyte-my
50	180	9.8	368	1	BGHUN	biglycan precursor
51	179.5	9.8	440	2	A39613	oligodendrocyte-my
52	179.5	9.8	1469	2	B36655	slit protein 2 pre
53	179.5	9.8	1480	2	A36655	slit protein 1 pre
54	179	9.8	1039	2	T22117	hypothetical prote
55	176.5	9.8	1268	2	A49674	flilghtless-1 homol
56	176.5	9.8	1112	2	T10504	disease resistance
57	176	9.6	653	2	T25194	hypothetical prote
58	176	9.6	864	2	T08575	protein kinase hom
59	175	9.5	858	2	T00258	hypothetical prote
60	174	9.5	462	2	D84858	hypothetical prote
61	172.5	9.4	404	2	T08549	hypothetical prote
62	172	9.4	361	2	A53860	chondroadherin pre
63	171.5	9.4	626	1	NBRH1A	platelet glycoprot
64	171.5	9.4	682	2	A49121	cell-surface molec
65	171.5	9.4	682	2	A43318	connectin precursor
66	171	9.4	375	2	S05390	fibronectin precu
67	171	9.4	376	2	S55275	fibronectin precu
68	170.5	9.3	1143	2	T10636	hypothetical prote
69	169	9.2	964	2	T49038	hypothetical prote
70	168	9.2	395	2	T01392	leucine-rich repea
71	167	9.1	603	2	T24315	hypothetical prote
72	167	9.1	851	2	S67285	NUP1 protein - yea
73	167	9.1	855	2	T17460	disease resistance
74	166.5	9.1	562	2	T34319	hypothetical prote
75	166.5	9.1	567	2	T46210	hypothetical prote
76	165.5	9.1	1115	2	S40241	G protein-coupled
77	165	9.0	1143	2	B84431	probable receptor
78	165	9.0	1535	2	S46224	peroxidasein - fru
79	165	9.0	2493	2	A55481	adenylate cyclase
80	164.5	9.0	549	2	T41744	hypothetical prote
81	164.5	9.0	679	2	T28713	hypothetical prote
82	164	9.0	420	2	A53531	oncofetal tropobol
83	164	9.0	740	2	B84741	hypothetical prote
84	163	8.9	1025	2	T42626	secreted leucine-r
85	163	8.9	1839	1	OVBVK	adenylate cyclase
86	162	8.9	2026	1	OVBVK	adenylate cyclase
87	160	8.8	528	2	T15198	hypothetical prote
88	160	8.8	1134	2	T04587	hypothetical prote
89	159.5	8.7	559	2	T42998	Ras-binding protei
90	159	8.7	382	2	T39068	proline-arginine-
91	158.5	8.7	478	2	H86459	hypothetical prote
92	158.5	8.7	480	2	T00971	probable disease r
93	158.5	8.7	809	2	B84631	probable receptor-
94	158	8.6	768	2	T17462	disease resistance
95	158	8.6	1097	2	A29943	Toll protein precu
96	158	8.6	1192	2	T48499	receptor-like prot
97	157	8.6	157	2	IS6258	RPI05 - mouse
98	157	8.6	1025	1	A57676	protein kinase Xa2
99	156.5	8.6	572	2	T30947	hypothetical prote
100	156.5	8.6	613	2	A88684	protein AC7.2 (lmp
101	156.5	8.6	863	2	A55173	cf-9 protein precu
102	155.5	8.5	380	2	S71876	fibronectin - chi

103	154.5	8.5	976	2	B84659	probable receptor-
104	154	8.4	720	2	T02361	hypothetical prote
105	154	8.4	890	2	T00800	disease resistance
106	153.5	8.4	771	2	T02565	disease resistance
107	153.5	8.4	994	2	H96510	probable disease r
108	153	8.4	538	2	T01102	disease resistance
109	153	8.4	800	2	G84740	hypothetical prote
110	153	8.4	925	2	C84538	probable LRR recep
111	153	8.4	1027	2	B85089	receptor protein k
112	152.5	8.3	224	2	T32185	hypothetical prote
113	152.5	8.3	540	2	T12704	leucine-rich prote
114	152	8.3	612	2	T10727	protein kinase Xa2
115	151.5	8.3	905	2	T00475	probable disease r
116	151.5	8.3	1338	2	T23007	hypothetical prote
117	151	8.3	380	2	T01281	probable leucine-r
118	151	8.3	855	2	T07015	Cf-4A protein - to
119	150.5	8.2	683	2	T24486	hypothetical prote
120	150.5	8.2	1002	2	T24603	receptor protein k
121	150	8.2	326	2	T24722	hypothetical prote
122	149.5	8.2	432	2	F86263	hypothetical prote
123	149.5	8.2	980	2	H84632	probable receptor-
124	149	8.2	335	2	H84616	protein F21B7.6 (l
125	149	8.2	397	2	T00914	leucine-rich repa
126	147	8.0	382	2	T04260	hypothetical prote
127	147	8.0	800	2	S37387	internalin A (limp
128	147	8.0	800	2	AB1129	protein kinase hom
129	147	8.0	1029	2	T00712	hypothetical prote
130	147	8.0	1068	2	H96769	hypothetical prote
131	147	8.0	1784	2	C96615	hypothetical prote
132	146.5	8.0	717	2	T33395	protein F3M18.12 (
133	146.5	8.0	996	2	F86410	hypothetical prote
134	146.5	8.0	1232	2	T05322	hypothetical prote
135	146	8.0	554	2	T23841	probable receptor-
136	146	8.0	830	2	B84846	hypothetical prote
137	145.5	8.0	332	2	H84527	protein F2G5.26 (l
138	145.5	8.0	677	2	H86208	hypothetical prote
139	145	7.9	448	2	T27395	protein kinase hom
140	145	7.9	1029	2	T05050	brassinosteroid-in
141	145	7.9	1196	2	T09356	monocyte surface g
142	144.5	7.9	1025	2	T45647	receptor protein k
143	144.5	7.9	960	2	G84652	probable receptor-
144	143.5	7.8	298	2	UC4130	osteoeglycin precu
145	143	7.8	596	2	AE1515	internalin like pr
146	143	7.8	818	2	T01105	disease resistance
147	143	7.8	907	2	A86460	99.9K hypothetical
148	143	7.8	702	2	T21148	hypothetical prote
149	142.5	7.8	981	2	TS0851	receptor protein k
150	142.5	7.8	2145	2	UC4747	adenylate cyclase
151	142	7.8	864	2	D84740	adenylate cyclase
152	142	7.8	1692	2	A33988	hypothetical prote
153	142	7.8	800	2	H84740	probable disease r
154	141.5	7.7	869	2	A71400	hypothetical prote
155	141	7.7	1120	2	B86479	receptor protein k
156	140.5	7.7	987	2	TS0860	hypothetical prote
157	140	7.7	1120	2	TS0860	receptor protein k
158	139	7.6	610	2	T23836	hypothetical prote
159	138.5	7.6	818	2	F96586	hypothetical prote
160	138.5	7.6	1019	2	C96519	probable disease r
161	138	7.5	322	2	S72271	proteoglycan lb pr
162	138	7.5	486	2	B86460	hypothetical prote
163	138	7.5	932	2	T84849	receptor-like prote
164	138	7.5	988	2	T45717	receptor-kinase 11
165	138	7.5	1088	2	E86312	filae.9 protein -
166	137.5	7.5	598	2	C96756	receptor-like prot
167	137.5	7.5	605	2	AG0123	probable antigenic
168	137.5	7.5	853	2	T17461	disease resistance
169	137.5	7.5	910	2	G84648	probable disease r
170	137.5	7.5	1152	2	T31911	hypothetical prote
171	137	7.5	409	2	T43589	Yop targeted effec
172	136.5	7.5	397	2	S49301	AMU1175 protein -
173	136.5	7.5	419	2	T49292	hypothetical prote
174	136.5	7.5	505	2	AC1469	internalin like pr
175	136.5	7.5	845	2	T07039	Hcr9-0 protein - t
176	136.5	7.5	1109	2	T18535	receptor-like prot
177	136.5	7.5	1166	2	F96598	protein F20N2.4 (l
178	136	7.5	983	2	G84524	probable disease r
179	136	7.4	999	1	S27756	receptor-like prote
180	136	7.4	1123	2	D96756	receptor-like prote
181	135.5	7.4	766	2	T01817	hypothetical prote
182	135.5	7.4	992	2	T05335	hypothetical prote
183	135.5	7.4	1016	2	T30653	disease resistance
184	135	7.4	316	2	A41781	proteoglycan-lb -
185	135	7.4	371	2	T49908	hypothetical prote
186	135	7.4	962	2	T04124	receptor-like prote
187	135	7.4	1133	2	E86308	AMU118 protein -
188	134.5	7.4	500	2	S49302	hypothetical prote
189	134.5	7.4	568	2	F86291	hypothetical prote
190	134	7.3	421	2	T45266	probable receptor-
191	134	7.3	1007	2	C84568	protein kinase Xa2
192	133.5	7.3	996	2	T10725	probable receptor-
193	133.5	7.3	1124	2	B84742	hypothetical prote
194	133	7.3	391	2	T04609	hypothetical prote
195	133	7.3	499	2	D83333	protein kinase Xa2
196	133	7.3	813	2	T04313	hypothetical prote
197	133	7.3	889	2	T20123	hypothetical prote
198	132.5	7.2	910	2	G02020	p37NB - human
199	132	7.2	313	2	UC7361	foliitropin recept
200	132	7.2	696	2	C84524	probable disease r
201	132	7.2	1011	2	AC38971	polycystic kidney
202	132	7.2	4302	2	T46170	disease resistance
203	131.5	7.2	904	2	T46170	hypothetical prote
204	131	7.2	305	2	UC7361	ipah protein - Shi
205	131	7.2	574	2	T05887	protein kinase hom
206	131	7.2	976	2	T05887	hypothetical prote
207	131	7.2	1003	2	T05888	tsu-1 homolog - hu
208	130.5	7.1	277	2	G86459	Hypothetical 55.6
209	130	7.1	342	2	S23764	polygalacturonase-
210	129.5	7.1	512	2	S23764	hypothetical prote
211	129.5	7.1	419	2	A90888	hypothetical prote
212	129.5	7.1	419	2	H85779	hypothetical prote
213	129.5	7.1	613	2	T15349	hypothetical prote
214	129.5	7.1	890	2	C96654	hypothetical prote
215	129.5	7.1	1013	2	T10659	probable serine/th
216	129	7.1	277	2	S25770	probable RSP-1 pro
217	129	7.1	1223	2	E88451	protein K10D2.1 (l
218	128.5	7.0	921	2	B86234	hypothetical prote
219	128.5	7.0	1064	2	B86465	hypothetical prote
220	128	7.0	886	2	C84517	probable receptor-
221	128	7.0	1079	2	C96772	probable antigenic
222	127.5	7.0	626	2	AE0123	hypothetical prote
223	127.5	7.0	719	2	T47727	osteoinductive fac
224	127	6.9	298	2	T35259	probable disease r
225	127	6.9	835	2	T05259	hypothetical prote
226	127	6.9	1008	2	D84434	hypothetical prote
227	127	6.9	1286	2	T13476	probable antigenic
228	126.5	6.9	291	2	AF0123	hypothetical prote
229	126.5	6.9	333	2	T34555	osteoinductive fac
230	126	6.9	299	2	A35272	hypothetical prote
231	126	6.9	364	2	T08903	hypothetical prote
232	126	6.9	729	2	F86308	similar to disease
233	126	6.9	977	2	C96745	hypothetical prote
234	126	6.9	1131	2	F86662	hypothetical prote
235	125.5	6.9	311	2	B86211	hypothetical prote
236	125.5	6.9	621	2	T39204	probable LRR recep
237	125.5	6.9	767	2	B84594	G protein-coupled
238	125.5	6.9	925	2	UC2033	hypothetical prote
239	125	6.8	431	2	T04868	probable disease r
240	125	6.8	741	2	T05250	protein kinase hom
241	125	6.8	980	2	T05444	receptor-kinase 11
242	125	6.8	1011	2	T45718	suppressor protein
243	125	6.8	338	2	S38030	internalin, probab
244	124.5	6.8	666	2	A11174	probable disease r
245	124.5	6.8	668	2	T05257	hypothetical prote
246	124.5	6.8	849	2	C97303	internalin, probab
247	124.5	6.8	851	2	AD1437	
248	124	6.8	360	2	S68205	ss622 protein homo

249	124	6.8	473	2	D85041	hypothetical prote	322	111	6.1	612	2	I73633	gene tixC protein
250	123.5	6.8	670	2	H96707	probable receptor	323	111	6.1	661	2	C85282	hypothetical prote
251	123	6.7	218	2	T01104	disease resistance	324	111	6.1	707	2	T28418	ORF MSV257 leucine
252	123	6.7	432	2	E96712	unknown protein, 6	325	111	6.1	825	2	A55178	neurotrophin recep
253	123	6.7	728	2	D86278	hypothetical prote	326	111	6.1	835	2	I73632	neurotrophin-3-rec
254	123	6.7	1045	2	T41119	internalin - relate	327	111	6.1	943	1	E84429	probable receptor-
255	122.5	6.7	630	2	S13724	ESAG 8 protein - T	328	110.5	6.0	494	2	B96534	hypothetical prote
256	122.5	6.7	743	2	C84633	probable disease r	329	110.5	6.0	695	2	I45896	follicle stimulat
257	122	6.7	268	2	T19697	hypothetical prote	330	110.5	6.0	855	2	T05981	hypothetical prote
258	122	6.7	367	2	A33950	YopM protein - Yer	331	110.5	6.0	874	2	E97302	hypothetical prote
259	122	6.7	990	2	T03784	probable receptor	332	110.5	6.0	594	2	T48216	hypothetical prote
260	121.5	6.6	391	2	S49300	AMW1236 protein -	333	110	6.0	573	2	A85357	receptor-like kina
261	121.5	6.6	674	2	S59476	kinase-like transm	334	110	6.0	646	2	B84852	probable receptor-
262	121	6.6	808	2	B97303	hypothetical prote	335	110	6.0	699	2	T15920	hypothetical prote
263	121	6.6	1495	2	T131434	denzin-180 - rat	336	110	6.0	1237	2	AC1583	internalin protein
264	120.5	6.6	329	2	T17033	leucine rich repea	337	109.5	6.0	388	2	AF1383	internalin protein
265	120.5	6.6	630	2	A36359	VSG expression sit	338	109.5	6.0	947	2	G86420	probable receptor-
266	120.5	6.6	951	2	A96770	hypothetical prote	339	109.5	6.0	1731	2	AB3045	hypothetical prote
267	120	6.6	694	2	UC2237	foliitropin recept	340	109.5	6.0	1731	2	B96241	receptor-like kina
268	119.5	6.5	191	2	E84740	hypothetical prote	341	109.5	6.0	2327	2	T42630	hypothetical prote
269	119.5	6.5	567	2	H84770	probable receptor-	342	109	6.0	735	2	T00850	hypothetical prote
270	119.5	6.5	581	2	G96811	unknown protein T1	343	109	6.0	764	2	A40077	receptor kinase-li
271	119.5	6.5	607	2	C84630	probable LRR recep	344	109	6.0	978	2	E96787	receptor kinase-li
272	119.5	6.5	991	2	T52400	receptor-like prot	345	109	6.0	1009	2	T45645	hypothetical prote
273	118.5	6.5	699	2	T05225	extensin homolog F	346	109	6.0	1095	2	G96746	hypothetical prote
274	118.5	6.5	766	2	G86308	similar to disease	347	108.5	5.9	173	2	T47176	hypothetical prote
275	118	6.5	349	2	T15422	hypothetical prote	348	108.5	5.9	474	1	B39667	brain-derived neur
276	117.5	6.4	176	1	A46606	platelet glycoprot	349	108.5	5.9	476	1	B39667	brain-derived neur
277	117.5	6.4	383	2	B86272	protein F16A1.12	350	108.5	5.9	654	2	C87587	hypothetical prote
278	117.5	6.4	656	2	AE1479	receptor-like surf	351	108.5	5.9	821	1	A39667	brain-derived neur
279	117.5	6.4	662	2	T46005	receptor-like prot	352	108.5	5.9	839	2	T04859	extensin homolog F
280	117	6.4	885	2	B86257	NBS/LRR disease re	353	108.5	5.9	967	2	G96637	hypothetical prote
281	116.5	6.4	645	2	T05251	probable disease r	354	108	5.9	764	2	I48882	probable receptor-
282	116.5	6.4	1234	2	T15415	hypothetical prote	355	108	5.9	920	2	F86420	hypothetical prote
283	115.5	6.3	318	2	B64900	probable polygalac	356	107.5	5.9	389	2	H86266	hypothetical prote
284	115.5	6.3	327	2	T02653	probable polygalac	357	107.5	5.9	902	2	T00588	hypothetical prote
285	115.5	6.3	548	2	AH1107	internalin H limpo	358	107	5.9	307	2	S36779	cytochrome c P303
286	115.5	6.3	671	2	D84648	probable disease r	359	107	5.9	467	2	G83266	hypothetical prote
287	115.5	6.3	695	2	UC1493	foliitropin recept	360	107	5.9	499	2	H87460	hypothetical prote
288	115.5	6.3	716	2	H84421	probable receptor-	361	107	5.9	618	2	T48193	hypothetical prote
289	115.5	6.3	942	1	JQ1674	protein kinase TMK	362	107	5.9	1121	2	A82809	exodeoxyribonuclea
290	115.5	6.3	1109	2	C84545	probable disease r	363	107	5.9	2944	2	A54849	collagen alpha 1(V
291	115	6.3	940	2	H86420	probable receptor-	364	106.5	5.8	670	2	T00083	hypothetical prote
292	115	6.3	985	2	T06049	hypothetical prote	365	106.5	5.8	886	2	T40734	probable adenylate
293	114.5	6.3	756	2	C87432	hypothetical prote	366	106	5.8	499	2	AT1107	internalin E limpo
294	114.5	6.3	1112	2	T00952	hypothetical prote	367	106	5.8	521	2	AC1949	hypothetical prote
295	114.5	6.3	1219	2	T06608	disease resistance	368	106	5.8	2062	2	G96602	probable receptor
296	114	6.2	327	2	S47965	monocyte surface g	369	105.5	5.8	719	2	F96577	hypothetical prote
297	114	6.2	366	1	TDMSM4	hypothetical prote	370	105.5	5.8	760	2	T06291	extensin homolog T
298	114	6.2	966	2	D96662	hypothetical prote	371	105.5	5.8	919	2	T05746	hypothetical prote
299	114	6.2	2224	1	KFHU5	coagulation factor	372	105.5	5.8	921	2	D86293	F7H2.22 protein -
300	113.5	6.2	786	2	T01456	extensin homolog F	373	105.5	5.8	942	2	C96574	hypothetical prote
301	113.5	6.2	830	2	C86181	hypothetical prote	374	105	5.7	332	2	S43988	protein phosphatas
302	113.5	6.2	833	2	B85035	hypothetical prote	375	105	5.7	587	2	AC1510	internalin protein
303	113	6.2	518	2	S50465	PAC2 protein - yea	376	105	5.7	673	2	AF1143	internalin protein
304	113	6.2	374	2	A34548	foliitropin recept	377	105	5.7	892	1	JN0898	foliitropin recept
305	113	6.2	1240	2	T06404	resistance complex	378	105	5.7	695	2	T08973	probable serine/th
306	112.5	6.2	630	1	BMUT80	regulatory protein	379	104.5	5.7	744	2	E86255	hypothetical prote
307	112.5	6.2	702	2	A86383	76 kD protein kina	380	104.5	5.7	764	2	A35956	thyrotropin recept
308	112.5	6.2	1340	2	A39908	proteoglycan core	381	104.5	5.7	788	2	AC0786	secreted effector
309	112	6.1	589	2	AB1151	internalin protein	382	104.5	5.7	1021	2	AB6421	receptor-like seri
310	112	6.1	660	2	T45569	receptor protein K	383	104	5.7	419	2	A40728	microphthalmia-ass
311	112	6.1	773	2	T00502	probable receptor-	384	104	5.7	695	1	ORHUFT	foliitropin recept
312	112	6.1	786	2	T08664	Toll protein-like	385	103.5	5.7	330	2	JQ2262	Polygalacturonase
313	112	6.1	821	2	AB1126	internalin, peptid	386	103.5	5.7	352	2	S49299	hypothetical prote
314	111.5	6.1	361	2	AH1469	internalin protein	387	103.5	5.7	509	2	T05260	hypothetical prote
315	111.5	6.1	431	2	T27904	hypothetical prote	388	103.5	5.7	538	2	T47624	hypothetical prote
316	111.5	6.1	449	2	G85332	hypothetical prote	389	103.5	5.7	589	2	T18239	transcription etfe
317	111.5	6.1	449	2	T10650	hypothetical prote	390	103.5	5.7	598	2	AB1236	internalin protein
318	111.5	6.1	825	2	A40026	neurotrophin-3 rec	391	103.5	5.7	617	2	S52797	multi protein - hum
319	111	6.1	227	2	T27905	hypothetical prote	392	103.5	5.7	847	2	F96531	hypothetical prote
320	111	6.1	414	2	C96770	hypothetical prote	393	103	5.6	419	2	I38024	MIRF protein - hum
321	111	6.1	547	2	T09912	hypothetical prote	394	103	5.6	1253	2	T45787	disease resistance

395	103	5.6	2479	2	P87386	conserved hypother
396	102.5	5.6	395	2	A46260	DSF100 protein pre
397	102.5	5.6	630	2	T31798	hypothetical prote
398	102.5	5.6	725	2	T01268	leucine-rich repa
399	102.5	5.6	727	2	C84534	hypothetical prote
400	102.5	5.6	766	2	B85440	receptor kinase-11
401	102	5.6	235	2	S15655	zein, 19K - maize
402	102	5.6	358	2	T01296	leucine-rich repa
403	102	5.6	411	2	AF2320	hypothetical prote
404	102	5.6	744	2	C84527	probable receptor-
405	102	5.6	774	2	D83208	probable ferredoxi
406	102	5.6	783	2	T45889	receptor protein X
407	102	5.6	860	2	C86203	hypothetical prote
408	102	5.6	865	2	B96553	hypothetical prote
409	102	5.6	1063	2	B96662	hypothetical prote
410	102	5.6	1063	2	S75071	hypothetical prote
411	101.5	5.6	296	2	AB1298	internalin C (lipo
412	101.5	5.6	419	2	H96695	hypothetical prote
413	101.5	5.6	852	2	T51259	tyrosine kinase C
414	101.5	5.6	979	2	D86574	hypothetical prote
415	101.5	5.6	1063	2	D86731	hypothetical prote
416	101	5.5	1064	2	JC4301	foliitropin recept
417	101	5.5	925	2	H96638	protein TIF9.20 [l
418	101	5.5	1095	2	T01916	hypothetical prote
419	101	5.5	1174	2	T08136	hypothetical prote
420	100.5	5.5	268	2	T45616	hypothetical prote
421	100.5	5.5	638	2	T05606	protein kinase hom
422	100	5.5	787	2	T27632	hypothetical prote
423	100	5.5	794	2	T27633	hypothetical prote
424	100	5.5	828	2	A88860	protein ZC518.3 [l
425	99.5	5.4	367	2	AC1338	internalin protein X
426	99.5	5.4	590	2	B86440	probable protein X
427	99.5	5.4	684	2	T01267	leucine-rich repa
428	99.5	5.4	797	2	T26207	hypothetical prote
429	99.5	5.4	892	2	T01899	disease resistance
430	99	5.4	187	2	T26726	hypothetical prote
431	99	5.4	435	2	I39171	cyclin A/CDX2-asso
432	99	5.4	858	2	B96602	hypothetical prote
433	99	5.4	1444	2	A54810	TMV resistance pro
434	99	5.4	1447	2	T42628	neuronal apoptosis
435	98.5	5.4	221	2	T07079	leucine-rich repa
436	98.5	5.4	719	2	T02154	protein kinase hom
437	98.5	5.4	889	2	B96637	hypothetical prote
438	98.5	5.4	898	2	E96659	hypothetical prote
439	98.5	5.4	1171	2	T12956	hypothetical prote
440	98	5.4	415	2	T13435	brain-derived neur
441	98	5.4	476	1	A35104	neurotrophin-3 rec
442	98	5.4	525	1	A58674	neurotrophin-3 rec
443	98	5.4	764	2	JC5643	thyroid stimulat
444	98	5.4	793	2	JC7390	neurotrophin-3 rec
445	98	5.4	803	1	S15695	brain-derived neur
446	98	5.4	821	1	B06943	brain-derived neur
447	98	5.4	1405	2	T04426	hypothetical prote
448	97.5	5.3	811	2	T48468	disease resistance
449	97.5	5.3	857	2	S44893	ice nucleation pro
450	97.5	5.3	951	2	T03511	probable disease r
451	97.5	5.3	957	2	E84547	hypothetical prote
452	97.5	5.3	1029	2	B96602	disease resistance
453	97.5	5.3	1217	2	T52348	hypothetical prote
454	97.5	5.3	2117	2	T36180	CDA peptide synthe
455	97	5.3	176	2	T23475	hypothetical prote
456	97	5.3	252	2	T01787	thyrotropin recept
457	97	5.3	343	2	JC1319	thyrotropin recept
458	97	5.3	343	2	G75381	hypothetical prote
459	97	5.3	381	2	S59943	early nodulin 8 pr
460	97	5.3	456	2	A31857	ribonuclease inhib
461	97	5.3	533	2	T52063	ran GTPase-activat
462	97	5.3	601	2	H96740	hypothetical prote
463	97	5.3	750	2	D86245	hypothetical prote
464	97	5.3	764	1	QRH0R8	thyrotropin recept
465	97	5.3	851	2	H84455	probable receptor-
466	97	5.3	2149	2	C96695	ribulose biphosph
467	96.5	5.3	343	2	C69019	conserved hypother

468	96.5	5.3	452	2	T46147	zinc finger protei
469	96.5	5.3	530	2	S37471	capid protein - N
470	96.5	5.3	532	2	A35149	lign protein - Shi
471	96.5	5.3	647	2	T05585	hypothetical prote
472	96.5	5.3	688	2	T04568	protein kinase hom
473	96.5	5.3	940	2	AB1744	internalin protein
474	96.5	5.3	1715	2	T06145	disease resistance
475	96	5.3	263	1	Z1ZM21	22K zein precursor
476	96	5.3	266	2	B22831	22K zein precursor
477	96	5.3	266	2	D97302	hypothetical prote
478	96	5.3	334	2	T05201	hypothetical prote
479	96	5.3	1036	2	E96682	hypothetical prote
480	96	5.3	1179	2	T04584	TMV resistance pro
481	95.5	5.2	630	2	AC1129	internalin B (lipo
482	95.5	5.2	1027	2	I38759	zinc finger/leucin
483	95	5.2	387	2	AD2057	DNA polymerase III
484	95	5.2	388	2	B70878	probable transfera
485	95	5.2	477	1	T73631	brain-derived neur
486	95	5.2	520	1	S44099	brain-derived neur
487	95	5.2	593	1	X1Z7FG	brain-derived neur
488	95	5.2	672	2	B84782	probable receptor-
489	95	5.2	799	1	BVKW21	zyg1 protein - Ca
490	95	5.2	818	1	S44098	brain-derived neur
491	95	5.2	822	1	A56853	brain-derived neur
492	95	5.2	1294	2	T18546	flax rust resist
493	95	5.2	6420	2	T30283	polyketide synthas
494	94.5	5.2	174	2	S43889	AKU3 protein - wh
495	94.5	5.2	511	2	T43382	alpel1 protein - fi
496	94.5	5.2	893	2	H96651	protein T3P18.19 [
497	94.5	5.2	956	2	T52414	H+-exporting ATPas
498	94.5	5.2	1007	2	T47430	disease resistance
499	94.5	5.2	1093	2	I38533	AF17 protein - hum
500	94.5	5.2	1590	2	B86398	protein TTN9.24 [l

## ALIGNMENTS

RESULT 1  
T14791  
hypothetical protein DKFZP586E011.1 - human (fragment)

C:Species: Homo sapiens (man)  
C:Date: 20-Sep-1999 #Sequence: revision 20-Sep-1999 #next\_change 20-Sep-1999

C:Accession: T14791  
R:Kocher, K.; Beyer, A.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, August 1999  
A:Reference number: Z18180

A:Accession: T14791  
A:Status: preliminary

A:Residues: 1-242 <KOB>  
A:Cross-references: EMBL:AL10276

A:Experimental source: adult uterus; clone DKFZP586E011  
A:Genetics:

A>Note: DKFZP586E011.1

Query Match 67.6%; Score 1235; DB 2; Length 242;  
Best Local Similarity 99.6%; Pred. No. 2, 2e-89;

Matches 241; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	112	SDLSHNGLTALPAESFTSSPLSDVNLSHNQREVSAFTTHSGRALHVDLSHNLIR	171
DB	1	SDLSHNGLTALPAESFTSSPLSDVNLSHNQREVSAFTTHSGRALHVDLSHNLIR	60
QY	172	LVHPFRAGAPAPPTIOSLNNRRLHAYVNDLPRLYISLDGNPLAVIGGAPAGGGL	231
DB	61	LVHPFRAGAPAPPTIOSLNNRRLHAYVNDLPRLYISLDGNPLAVIGGAPAGGGL	120
QY	232	THLSIASLQRLPELAPSGFRELPGIQVLDLSGNPKLNAGAEVBSGLSIOELDLSGNTL	291
DB	121	THLSIASLQRLPELAPSGFRELPGIQVLDLSGNPKLNAGAEVBSGLSIOELDLSGNTL	180
QY	292	VLPPEALLHLHPALQSVSVGQDVRCRLVREGTYYRRRGSSPKVPLHCVDRBSAAGPT	351





Db 245 NIDDEPTAI 253

# RESULT 4

JC7763

C/Species: Rattus norvegicus (Norway rat)  
C/Date: 01-Feb-2002 #sequence\_revision 01-Feb-2002 #text\_change 01-Feb-2002

C/Accession: JC7763

R/Fukunishi, K.; Matsuo, Y.; Kitanaka, C.; Kuchino, Y.; Tsuda, H.

Biochem. Biophys. Res. Commun. 287, 257-263, 2001

A/Title: Rat neuronal leucine-rich repeat protein-3: Cloning and regulation of the gene

A/Reference number: JC7763; PMID:11549284

A/Contents: Fibrosarcoma cells

A/Accession: JC7763

A/Molecule type: mRNA

A/Residues: 1-707 <FUK>

A/Cross-references: GB:AF291437

C/Comment: This protein, a new member of the neuronal leucine-rich repeat protein family in protein-protein interaction and functions as a cell adhesion molecule or soluble ligand

C/Genetics:

A/Genes: nlxr-3

C/Keywords: cell adhesion

Query Match

Best Local Similarity 25.3%; Pred. No. 1.2e-12;

Matches 98; Conservative 59; Mismatches 154; Indels 68; Gaps 11;

Db

Qy

24

33

33

82

90

Db

Qy

141

150

Db

Qy

173

210

Db

Qy

213

268

Db

Qy

273

328

Db

Qy

328

388

Db

Qy

388

Db

Qy

388

Db

Qy

388

Best Local Similarity 29.8%; Pred. No. 5e-12;

Matches 89; Conservative 40; Mismatches 104; Indels 66; Gaps 9;

Db

Qy

6

15

Db

Qy

61

69

Db

Qy

121

103

Db

Qy

180

157

Db

Qy

240

196

Db

Qy

196

Db

Qy

196

Db

Qy

196

Db

Qy

196

Db

Qy

196

Db

Qy

196

Db

Qy

196

Db

Qy

196

Db

Qy

196

Db

Qy

196

Db

Qy

196

Db

Qy

196

Db

Qy

A/Accession: A47507  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: mRNA  
 A/Residues: 1-560 <RES>  
 A/Cross-references: GB:L11238; NID:G388759; PID:AAA03069.1; PID:G388760  
 C/Comment: This platelet membrane protein is a substrate for thrombin.  
 C/Comment: The amino end of the intact protein is blocked.  
 C/Comment: This protein is absent in Bernard-Soulier syndrome.  
 C/Genetics:  
 A/Gene: GDB:GPS  
 A/Cross-references: GDB:230236; OMIM:173511  
 A/Map position: 5pter-5qter  
 C/Superfamily: leucine-rich alpha-2-glycoprotein repeat homology  
 C/Keywords: blocked amino end; glycoprotein; platelet; tandem repeat; transmembrane prot

Query Match 13.5%; Score 247; DB 2; Length 560;  
 Best Local Similarity 28.6%; Pred. No. 1.6e-11;  
 Matches 112; Conservative 42; Mismatches 145; Indels 92; Gaps 14;

QY 7 LLLAVSAQOTR--PCPPGQC-----EVEITFGLFDSITRVDCSG-- 48  
 DB 6 LICAIVGLRAQPPPCPKCVRDAQSGGDVARIISALGL--PTNLTHILLFGVGRG 63  
 QY 49 -----PHIMPVP-----IPDTAHLDISNRL-----EWNES 76  
 DB 64 VLQSGSFGMTVLRMLMISDHSIAVAPGTFPSDLIKKT--LRLSRKIKTHLFGALLDKM 121  
 QY 77 VLAQPGYTTLAGLDSHNLTSISPTAPSRIRYESIDLSHNGITLPAESFTS----- 130  
 DB 122 VL-----LEQLFLDHNAHLRGIDQNMFOKLVNQLQELALNQMLDFPASPILFNTLENTKL 174  
 QY 131 SPDSVNLISH-----NQLREVSVSAFTTHSGRALHVDLSHNLHRLV 173  
 DB 175 LDISGNLTHLPKELLAGQAKLERLLHSNRLVSLDGLANSGLATLQEPHNRHRSIA 234  
 QY 174 PHPTPAGLPAPTIOSLNLMANRHLAVPN---LRDLPLRYISLDGNPLAVIPGAPAGLQG 230  
 DB 235 P---GAPDRPLNLSLTISRHLAFIPSAFLFHSNLTLLTFENPLAEIPGVLFGEIMG 291  
 QY 231 LTHSLASLQRLPRLASGRELPGLOVLDSGNPKLMAGAEVFGSLSSLOELDLSGTN 290  
 DB 292 LQELIMLRKIQ--LRTLPAAFRNLSRLRYLGVLTSPRLSALPGCAFQGLGLOVLALHSNG 350  
 QY 291 LVPLPEALLHLPALQSVSVQGVDCRRLVR 321  
 DB 351 LTLALPDGLRGGLRGKLRQVSLRRN-RLRALPR 380

## RESULT 7

NBH0A2  
 leucine-rich alpha-2-glycoprotein - human  
 C/Species: Homo sapiens (man)  
 C/Date: 27-Nov-1985 #sequence\_revision 27-Nov-1985 #text\_change 05-Dec-1998  
 C/Accession: A03211  
 R/Takahashi, N.; Takahashi, Y.; Putnam, F.W.  
 Proc. Natl. Acad. Sci. U.S.A. 82, 1906-1910, 1985  
 A/Title: Periodicity of leucine and tandem repetition of a 24-amino acid segment in the  
 A/Reference number: A03211; MUID:85166241; PMID:3856868  
 A/Accession: A03211  
 A/Molecule type: protein  
 A/Residues: 1-312 <TAK>  
 C/Comment: The function of this plasma protein is not known.  
 C/Superfamily: leucine-rich alpha-2-glycoprotein; leucine-rich alpha-2-glycoprotein repe  
 C/Keywords: duplication; glycoprotein; plasma; tandem repeat  
 F/58-81/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>  
 F/83-105/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>  
 F/106-129/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>  
 F/130-153/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>  
 F/154-177/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>  
 F/178-201/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>  
 F/202-225/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>  
 F/226-249/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>  
 F/262-309/Domain: proteoglycan carboxyl-terminal homology <PCH>

F/2/Binding site: carbohydrate (Thr) (covalent) #status experimental  
 F/8-21,266-294/Disulfide bonds: #status experimental  
 F/44,151,234,290/Binding site: carbohydrate (Asn) (covalent) #status experimental  
 F/271/Binding site: carbohydrate (Asn) (covalent) #status absent

Query Match 12.9%; Score 236.5; DB 1; Length 312;  
 Best Local Similarity 32.4%; Pred. No. 5e-11;  
 Matches 97; Conservative 34; Mismatches 109; Indels 59; Gaps 14;

QY 26 CEVEITFGLFDSITRVDCSGGLPIMPVPIPLDTAHLDISNRLQEMVNSVLAQPGYTT 85  
 DB 8 CCV-----FRSDHSGSISQ--PRAIEGYLADLVHLAVEFPNLTPLPAILQGA--SK 58  
 QY 86 LAGLDSHNLTSISPTAPSRIRYESIDLSHNGITLPAESF--TSSPLSVNLSNQLR 144  
 DB 59 LQELHSSNGLSLSPFELRPVQRLVLDLTNNALTGLPPGLFOASATLDTLVLENQLE 118  
 QY 145 EVSVSAFTTHSGRALHVDLSHNLHRLVPEPTRAGLPA--PTIOSLNMANRHLAVPN- 201  
 DB 119 VLEFVS--WHLGKALGHDLDSGNRLKLP-----GLANFTLTLTDGEGQLTTPD 171  
 QY 202 -LR-DLPLRYISLDGNPLAVIPGAPAGIGITLHSLASLQRLPELAPSGRELPGLQVL 259  
 DB 172 LIRGPIQLERLHLEGNKLVGLKDL-----LPQ-----PDLRYL 206  
 QY 260 DISGNPKLMAGAEVFGSLSSLOELDLSGTNVLPLPEALLHLPALQSVSVQ---DVR 315  
 DB 207 FLNNGN-KLARVAAGAFQGLRQIDMLDLSNNSLASVPEGVM-----ASLQGPWDMK 256

## RESULT 8

JCS239  
 insulin-like growth factor acid-labile chain - baboon  
 C/Species: Papio sp. (baboon)  
 C/Date: 17-Apr-1997 #sequence\_revision 09-May-1997 #text\_change 09-May-1997  
 C/Accession: JCS239  
 R/Delhanty, P.; Baxter, R.C.  
 Biochem. Biophys. Res. Commun. 227, 897-902, 1996  
 A/Title: The cloning and expression of the baboon acid-labile subunit of the insulin-l  
 A/Reference number: JCS239; MUID:97040714; PMID:8686027  
 A/Contents: liver  
 A/Accession: JCS239  
 A/Molecule type: mRNA  
 A/Residues: 1-605 <DEL>  
 C/Comment: This factor is structurally related to proinsulin and have insulin-like met

Query Match 12.8%; Score 234.5; DB 2; Length 605;  
 Best Local Similarity 34.3%; Pred. No. 1.7e-10;  
 Matches 82; Conservative 21; Mismatches 95; Indels 41; Gaps 8;

QY 63 LDISNRLQEMVNSVLAQPGYTTLAGLDSHNLTSISPTAPSRIRYESIDLSHNGTA 122  
 DB 271 LDISNHRVAGLLEDPF--PGLLGLRVLRSHNAISLSPRTBEDLHFLBELQGLGNRRIRQ 328  
 QY 123 LABESFTS--SPDSVNLISNQLREVSVSAFTTHSGRALHVDLSHNLHRLVPHPTPAGL 181  
 DB 329 LAERSEFGIGLEVTLLDHNQLEVKVAF-----L 359  
 QY 182 PAPTIOSLNMANRHLAVPN---LRDL-PLRYISLDGNPLAVIPGAPAGLGLTLHLSIA- 237  
 DB 360 GLTNVAVMNLSGNCIRNLPQGVFRGLGKLSHLESGCIGRRPRTFAGLSGLRLFLKD 419  
 QY 238 -SLQRLPELAPSGRELPGLQVLDSGNPKLMAGAEVFGSLSSLOELDLSGTNVLPLP 295  
 DB 420 NGIVGIEGDSIWGLAE--LLELDTLSN-QLTPLHPQDFQGLGKLELYLLSHNRLAEDP 474

## RESULT 9

AS8532  
 glial cell membrane glycoprotein LIG-1 precursor - mouse  
 C/Species: Mus musculus (house mouse)  
 C/Date: 11-Apr-1997 #sequence\_revision 11-Apr-1997 #text\_change 05-Nov-1999  
 C/Accession: AS8532



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 2, 2004, 16:18:07 ; Search time 39 Seconds

(Without alignments)  
2855.844 Million cell updates/sec

Title: US-10-017-390A-397

Perfect score: 1828  
Sequence: 1 MPWPLLLLVASGQTRPC.....KVELHCVDTRFSARSPITL 353

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 500 summaries

Database :

1: SPTRMBL\_25:\*  
2: sp\_archaea:\*  
3: sp\_bacteria:\*  
4: sp\_fungi:\*  
5: sp\_human:\*  
6: sp\_invertebrate:\*  
7: sp\_mammal:\*  
8: sp\_mbc:\*  
9: sp\_organelle:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1817	99.4	353	4	Q8WUA6
2	1815	99.3	353	4	Q9UUX6
3	1537	84.1	372	11	Q8CBK6
4	1235	67.6	242	4	Q9UG10
5	767	42.0	347	13	Q7ZU11
6	311.5	17.0	713	4	Q8N182
7	263	14.4	707	11	Q9ESY6
8	261	14.3	707	11	Q97860
9	261	14.3	707	11	Q8CBK6
10	258	14.1	363	11	Q8CBK7
11	254	13.9	708	4	Q9H3W5
12	254	13.9	733	5	Q24250
13	254	13.9	737	5	Q9VU51
14	252.5	13.8	1360	5	Q9NDU1
15	251.5	13.8	542	5	Q9Y4G6
16	250	13.7	347	4	Q8Y4P5

17	250	13.7	718	13	Q73675	073675 xenopus lae
18	249.5	13.6	1065	4	Q94898	Q94898 homo sapien
19	249	13.6	1050	5	Q9BN18	Q9BN18 dirosophila
20	248	13.6	708	4	Q81Y06	Q81Y06 homo sapien
21	247.5	13.5	673	11	Q8B3T0	Q8B3T0 mus musculu
22	247.5	13.5	673	11	Q8R2G5	Q8R2G5 mus musculu
23	247	13.5	1392	5	Q9VAD1	Q9VAD1 dirosophila
24	245.5	13.4	1300	5	Q9NKG6	Q9NKG6 mus musculu
25	244.5	13.4	673	11	Q9CZT5	Q9CZT5 mus musculu
26	244.5	13.4	1029	6	Q86EB2	Q86EB2 bos taurus
27	243.5	13.3	1535	5	Q9VDF0	Q9VDF0 dirosophila
28	239.5	13.1	1022	6	Q8HXV0	Q8HXV0 bos taurus
29	238.5	13.0	342	11	Q91XU1	Q91XU1 mus musculu
30	238.5	13.0	811	4	Q7S139	Q7S139 homo sapien
31	238	13.0	927	4	Q9UGS3	Q9UGS3 homo sapien
32	238	13.0	927	4	Q8N537	Q8N537 homo sapien
33	235	12.9	453	4	Q86XY1	Q86XY1 homo sapien
34	235	12.9	1039	5	Q86BL1	Q86BL1 dirosophila
35	234.5	12.8	1514	5	Q9NKB9	Q9NKB9 dirosophila
36	234.5	12.8	1514	5	Q9VUN0	Q9VUN0 dirosophila
37	234	12.8	532	5	Q96671	Q96671 dirosophila
38	234	12.8	532	5	Q9VU53	Q9VU53 dirosophila
39	232	12.7	606	4	Q9B220	Q9B220 homo sapien
40	232	12.7	1104	10	Q7XUG6	Q7XUG6 oryza sativ
41	231.5	12.7	1512	13	Q9DE36	Q9DE36 brachydantio
42	231	12.6	606	11	Q8BZD4	Q8BZD4 mus musculu
43	231	12.6	606	11	Q8BLC0	Q8BLC0 mus musculu
44	230.5	12.6	928	4	Q93YD7	Q93YD7 homo sapien
45	230.5	12.6	1091	11	P70193	P70193 mus musculu
46	230	12.6	1094	4	Q9BYB8	Q9BYB8 homo sapien
47	229	12.5	391	11	Q9D3X0	Q9D3X0 mus musculu
48	228	12.5	579	11	Q8OX72	Q8OX72 mus musculu
49	228.5	12.5	363	4	Q9H5G9	Q9H5G9 homo sapien
50	228.5	12.5	1295	5	Q8T0X1	Q8T0X1 bombyx mori
51	228.5	12.5	1530	13	Q9QWZ3	Q9QWZ3 xenopus lae
52	228	12.5	1471	5	Q9VQC0	Q9VQC0 dirosophila
53	227.5	12.4	1459	5	Q8WRE4	Q8WRE4 anopheles g
54	226.5	12.4	1093	4	Q96JAI	Q96JAI homo sapien
55	226	12.4	567	11	Q9QZU3	Q9QZU3 mus musculu
56	225	12.3	796	11	Q9WVCL	Q9WVCL rattus norv
57	225	12.3	1458	11	Q8CUG8	Q8CUG8 rattus norv
58	225	12.3	1530	11	Q9WUG5	Q9WUG5 rattus norv
59	225	12.3	1531	11	Q88279	Q88279 rattus norv
60	224	12.3	562	11	Q8R113	Q8R113 mus musculu
61	224	12.3	570	11	Q9PBB9	Q9PBB9 mus musculu
62	222	12.2	1474	11	Q8CUG9	Q8CUG9 rattus norv
63	222.5	12.2	605	4	Q8TAY0	Q8TAY0 homo sapien
64	222.5	12.2	1533	4	Q7S094	Q7S094 homo sapien
65	221.5	12.1	1030	6	Q865R8	Q865R8 sus scrofa
66	221.5	12.1	809	11	Q9DBY4	Q9DBY4 mus musculu
67	221.5	12.1	837	11	Q80TV0	Q80TV0 mus musculu
68	220	12.0	1521	11	Q9R1B9	Q9R1B9 mus musculu
69	220	12.0	1618	4	Q9U1I7	Q9U1I7 homo sapien
70	219.5	12.0	513	4	Q8EYH5	Q8EYH5 homo sapien
71	219.5	12.0	581	6	Q9BGP6	Q9BGP6 macaca fasc
72	219.5	12.0	1446	5	Q9V8Z0	Q9V8Z0 dirosophila
73	219	12.0	310	13	Q9BDZ8	Q9BDZ8 petromyzon
74	219	12.0	410	13	Q9DDZ7	Q9DDZ7 petromyzon
75	219	12.0	557	4	Q8N5V4	Q8N5V4 homo sapien
76	218.5	12.0	550	4	Q86CU4	Q86CU4 homo sapien
77	218.5	12.0	581	6	Q9SKT8	Q9SKT8 macaca fasc
78	218.5	12.0	603	11	Q70211	Q70211 rattus norv
79	218	11.9	406	11	Q8CJH0	Q8CJH0 rattus norv
80	218	11.9	611	11	Q7Y062	Q7Y062 mus musculu
81	218	11.9	1534	4	Q7S093	Q7S093 homo sapien
82	217	11.9	347	13	Q9DE00	Q9DE00 petromyzon
83	217	11.9	738	5	Q93373	Q93373 caenorhabdi
84	217	11.9	1531	11	Q9WVB5	Q9WVB5 mus musculu
85	217	11.9	1537	11	Q80TR4	Q80TR4 mus musculu
86	216	11.8	798	4	Q8WMZ2	Q8WMZ2 homo sapien
87	216	11.8	905	11	Q7TN18	Q7TN18 rattus norv
88	215.5	11.8	648	11	Q8V135	Q8V135 mus musculu
89	215.5	11.8	649	4	Q96A85	Q96A85 homo sapien

90	215.5	11.8	737	5	Q965M3	Q965m3 caenornabdi	153	195.5	10.7	581	10	Q04143	Q04143 silene latf
91	215.5	11.8	881	5	Q965M2	Q965m2 caenornabdi	154	195.5	10.7	633	11	Q08Y16	Q08Y16 mus musculu
92	215.5	11.8	1066	5	Q18902	Q18902 caenornabdi	155	195.5	10.7	633	11	Q08R03	Q08R03 mus musculu
93	215.5	11.8	1447	5	Q16779	Q16779 caenornabdi	156	195.5	10.7	669	11	Q08Y14	Q08Y14 mus musculu
94	215	11.8	514	11	Q08Z81	Q08z81 mus musculu	157	195.5	10.7	675	11	Q08BMT4	Q08bmt4 mus musculu
95	215	11.8	582	11	Q08GJ7	Q08gj7 mus musculu	158	195.5	10.7	721	11	Q08BUT7	Q08but7 mus musculu
96	215	11.8	1385	5	Q9V8Z5	Q9v8z5 mus musculu	159	195.5	10.7	742	5	Q08BUD4	Q08bud4 strongyloce
97	215	11.8	1389	5	Q24591	Q24591 drosophila	160	195.5	10.7	370	4	Q08N97	Q08n97 mus sapien
98	214.5	11.7	687	11	Q09J10	Q09j10 mus musculu	170	195	10.7	370	4	Q08N97	Q08n97 mus sapien
99	214	11.7	544	13	Q08UV23	Q08uv23 spheroioides	171	195	10.7	552	5	Q09V14	Q09v14 drosophila
100	213.5	11.7	614	6	Q09PE5	Q09pe5 homo sapien	172	195	10.7	799	5	Q09V64	Q09v64 drosophila
101	213.5	11.7	614	6	Q09N08	Q09n08 macaca fasc	173	194.5	10.6	577	4	Q08N35	Q08n35 homo sapien
102	213.5	11.7	652	11	Q09PH1	Q09ph1 mus musculu	174	194.5	10.6	1024	2	Q084I6	Q084i6 raiistonia s
103	213.5	11.7	653	4	Q09BMT	Q09bmt homo sapien	175	194	10.6	332	13	Q08QFN6	Q08qfn6 elaphe quad
104	213.5	11.7	923	4	Q08VU0	Q08vu0 homo sapien	176	194	10.6	515	11	Q08C91	Q08c91 mus musculu
105	212.5	11.6	716	11	Q061809	Q061809 mus musculu	177	194	10.6	515	11	Q08B33	Q08b33 mus musculu
106	212	11.6	613	4	Q725L7	Q725l7 homo sapien	178	194	10.6	528	11	Q08U08	Q08u08 mus musculu
107	212	11.6	1052	4	Q9V4C4	Q9v4c4 mus musculu	179	194	10.6	719	4	Q06N16	Q06n16 homo sapien
108	212	11.6	1523	11	Q9WVB4	Q9wvb4 mus musculu	180	194	10.6	719	4	Q06N16	Q06n16 homo sapien
109	211.5	11.6	359	13	Q09DE03	Q09de03 oreochromis	181	194	10.6	719	11	Q08BXA0	Q08bxa0 mus musculu
110	211.5	11.6	606	11	Q7TT38	Q7tt38 mus musculu	182	194	10.6	746	11	Q08B2L0	Q08b2l0 mus musculu
111	211.5	11.6	614	11	Q9D1T0	Q9d1t0 mus musculu	183	194	10.6	940	5	Q08T753	Q08t753 branchiosto
112	211	11.5	602	11	Q08S83	Q08s83 mus musculu	184	194	10.6	1051	5	Q24007	Q24007 drosophila
113	211	11.5	636	11	Q08K34	Q08k34 mus musculu	185	194	10.6	1076	5	Q08MT4	Q08mt4 drosophila
114	211	11.5	636	11	Q08XU8	Q08xu8 mus musculu	186	193.5	10.6	1051	5	Q09P29	Q09p29 drosophila
115	211	11.5	716	4	Q08YV5	Q08yv5 homo sapien	187	193	10.6	1051	5	Q09P29	Q09p29 drosophila
116	211	11.5	730	4	Q09P231	Q09p231 homo sapien	188	192.5	10.5	370	11	Q08B33	Q08b33 mus musculu
117	211	11.5	1012	5	Q09Y17	Q09y17 asterina pe	189	192	10.5	399	11	Q08B45	Q08b45 mus musculu
118	211	11.5	1280	5	Q09Y17	Q09y17 asterina pe	190	192	10.5	577	13	Q08AV14	Q08av14 xenopus lae
119	210.5	11.5	518	11	Q08XG9	Q08xg9 mus musculu	191	192	10.5	1778	16	Q08Y32	Q08y32 listeria mo
120	210.5	11.5	591	11	Q08Z80	Q08z80 mus musculu	192	191.5	10.5	311	16	Q08F16	Q08f16 leprospira
121	210.5	11.5	1523	11	Q08Z80	Q08z80 mus musculu	193	191.5	10.5	565	11	Q08C030	Q08c030 mus musculu
122	210	11.5	582	11	Q08Z80	Q08z80 mus musculu	194	191.5	10.5	878	11	Q08KX9	Q08kx9 mus musculu
123	210	11.5	739	11	Q08KX5	Q08kx5 mus musculu	195	191	10.4	402	4	Q08N641	Q08n641 homo sapien
124	210	11.5	836	10	Q09C14	Q09c14 brachydando	196	190.5	10.4	516	4	Q03300	Q03300 homo sapien
125	209.5	11.5	373	13	Q0803T1	Q0803t1 petromyzon	197	190.5	10.4	518	13	Q07SYC0	Q07syco brachydando
126	208	11.4	388	5	Q09DZ9	Q09dz9 caenornabdi	198	189.5	10.4	677	10	Q08RUT5	Q08rut5 oryza sativ
127	208	11.4	602	13	Q093377	Q093377 caenornabdi	199	189.5	10.4	947	10	Q08RT5	Q08rt5 oryza sativ
128	207.5	11.4	548	5	Q09VU1	Q09vu1 drosophila	200	189.5	10.4	628	4	Q08CPN7	Q08cpn7 elaphe quad
129	207.5	11.4	640	4	Q09HC12	Q09hc12 homo sapien	201	189.5	10.4	785	4	Q09P263	Q09p263 homo sapien
130	207.5	11.4	640	11	Q08C031	Q08c031 mus musculu	202	189	10.3	332	13	Q08CPN7	Q08cpn7 elaphe quad
131	207.5	11.4	640	11	Q08C031	Q08c031 mus musculu	203	189	10.3	785	4	Q09P263	Q09p263 homo sapien
132	207.5	11.4	273	4	Q09NU4	Q09nu4 homo sapien	204	189	10.3	1036	10	Q09N37	Q09n37 aradidopsis
133	206.5	11.3	615	5	Q09Z84	Q09z84 drosophila	205	188.5	10.3	499	10	Q08YV9	Q08yv9 aradidopsis
134	206	11.3	622	4	Q72ZQ7	Q72zq7 homo sapien	206	188	10.3	329	5	Q09YF8	Q09yf8 drosophila
135	205	11.2	491	5	Q09VK6	Q09vk6 drosophila	207	188	10.3	1179	6	Q09B86	Q09b86 macaca fasc
136	205	11.2	1079	6	Q0865B9	Q0865b9 caris famli	208	187.5	10.3	522	4	Q096DN1	Q096dn1 homo sapien
137	204.5	11.2	601	4	Q096CX1	Q096cx1 homo sapien	209	187.5	10.3	522	4	Q096DN1	Q096dn1 homo sapien
138	204	11.2	582	11	Q08EVL0	Q08evl0 mus musculu	210	187.5	10.3	626	11	Q08LY3	Q08ly3 mus musculu
139	204	11.2	1515	13	Q09DE37	Q09de37 brachydando	211	187.5	10.3	649	11	Q08BGT1	Q08bgt1 mus musculu
140	204	11.2	1529	13	Q72X12	Q72x12 xenopus lae	212	187.5	10.3	893	4	Q096C25	Q096c25 homo sapien
141	203.5	11.1	1031	6	Q08H52	Q08h52 felis silve	213	187.5	10.3	910	4	Q09H75	Q09h75 homo sapien
142	203	11.1	524	5	Q08R378	Q08r378 mus musculu	214	187.5	10.3	1247	5	Q09B86	Q09b86 macaca fasc
143	203	11.1	524	5	Q23580	Q23580 caenornabdi	215	187.5	10.3	1756	5	Q09B86	Q09b86 macaca fasc
144	202.5	11.1	601	4	Q09HC24	Q09hc24 homo sapien	216	187.5	10.3	1756	5	Q09B86	Q09b86 macaca fasc
145	202	11.1	581	4	Q09BTR7	Q09btr7 homo sapien	217	187.5	10.3	1756	5	Q09B86	Q09b86 macaca fasc
146	202	11.1	602	4	Q09H9A6	Q09h9a6 homo sapien	218	187	10.2	554	5	Q09VDD5	Q09vdd5 drosophila
147	201.5	11.0	526	10	Q07XJ53	Q07xj53 aradidopsis	219	186.5	10.2	770	10	Q09F15	Q09f15 aradidopsis
148	201.5	11.0	680	5	Q093374	Q093374 caenornabdi	220	186.5	10.2	1173	5	Q09V78	Q09v78 drosophila
149	201.5	11.0	1259	11	Q08BXA7	Q08bxa7 mus musculu	221	186	10.2	420	4	Q086UN3	Q086un3 homo sapien
150	201	11.0	961	5	P90920	P90920 caenornabdi	222	184.5	10.1	471	10	Q09LVR8	Q09lvr8 aradidopsis
151	200.5	11.0	470	5	Q09V354	Q09v354 drosophila	223	184	10.1	287	5	Q09M2B9	Q09m2b9 streptococ
152	200	10.9	1077	5	Q09NUG7	Q09nug7 drosophila	224	184	10.1	420	11	Q08OWD1	Q08owd1 raius novy
153	199	10.9	1119	16	Q08Z0H2	Q08z0h2 anabaena sp	225	184	10.1	633	16	Q08F3F6	Q08f3f6 leprospira
154	198.5	10.9	741	5	Q09VJA9	Q09vja9 drosophila	226	183.5	10.0	521	11	Q08BNA1	Q08bna1 mus musculu
155	198	10.8	364	11	Q08B551	Q08b551 mus musculu	227	183.5	10.0	597	5	Q09V09	Q09v09 aradidopsis
156	198	10.8	953	5	Q09V701	Q09v701 drosophila	228	183	10.0	785	10	Q09V09	Q09v09 aradidopsis
157	198	10.8	1346	5	Q09V477	Q09v477 drosophila	229	183	10.0	1275	16	Q09V09	Q09v09 aradidopsis
158	197.5	10.8	894	5	Q09BUD6	Q09bud6 strongyloce	230	183	10.0	1275	16	Q09V09	Q09v09 aradidopsis
159	197.5	10.8	1152	5	Q08RMS	Q08rms anopheles g	231	183	10.0	1275	16	Q09V09	Q09v09 aradidopsis
160	196.5	10.7	1221	5	Q09BIM9	Q09bim9 caenornabdi	232	183	10.0	1275	16	Q09V09	Q09v09 aradidopsis
161	196.5	10.7	1221	5	Q09BIM9	Q09bim9 caenornabdi	233	183	10.0	1275	16	Q09V09	Q09v09 aradidopsis
162	195.5	10.7	372	13	Q07T2W3	Q07t2w3 brachydando	234	182.5	10.0	423	16	Q08F751	Q08f751 leprospira
							235	182.5	10.0	440	11	Q07T25	Q07t25 raius novy



236	182.5	10.0	440	11	Q7TMM3	Q7Tm3 ratius novr	309	171.5	9.4	537	5	Q9VE49	Q9ve49 dirosophila
237	182.5	10.0	522	11	Q8K377	Q8K377 mus musculu	310	171.5	9.4	550	10	Q9AX18	Q9ax18 oryza sativ
238	182.5	10.0	535	10	Q8X350	Q8x350 braesia ni	311	171.5	9.4	586	5	Q21164	Q21164 caenornabdi
239	182.5	10.0	1356	5	Q8WR82	Q8wr82 anopheles g	312	171.5	9.4	626	4	Q8N1P3	Q8n1p3 homo sapien
240	182	10.0	492	11	Q99KT6	Q99kt6 mus musculu	313	171.5	9.4	626	4	Q8NG39	Q8ng39 homo sapien
241	181.5	9.9	584	10	Q49751	Q49751 arabidopsis	314	171.5	9.4	682	5	Q9VZ74	Q9vz74 dirosophila
242	181.5	9.9	584	10	Q8L722	Q8l722 arabidopsis	315	171.5	9.4	1002	10	Q9ARQ7	Q9arq7 oryza sativ
243	181.5	9.9	915	11	Q9ERV7	Q9erv7 mus musculu	316	171.5	9.4	1101	10	Q9FML8	Q9fm18 oryza sativ
244	181.5	9.9	1028	6	Q85E87	Q85e87 sus scrofa	317	171.5	9.4	1101	10	Q7XDJ5	Q7xdj5 oryza sativ
245	181.5	9.9	1135	10	Q7X511	Q7x511 oryza sativ	318	171	9.4	954	5	Q9VJ07	Q9vj07 dirosophila
246	181	9.9	853	11	Q8CB40	Q8cb40 mus musculu	319	171	9.4	2964	5	Q81VW7	Q81vw7 dictyosteli
247	181	9.9	1076	5	Q8MQU7	Q8mqu7 aedes aegy	320	170.5	9.3	584	10	Q49750	Q49750 arabidopsis
248	180.5	9.9	224	13	Q9D501	Q9d501 brachydantio	321	170.5	9.3	601	13	Q7SXM3	Q7sxm3 dirosophila
249	180.5	9.9	343	5	Q9WZ17	Q9wz17 dirosophila	322	170.5	9.3	892	5	P91644	P91644 dirosophila
250	180.5	9.9	426	16	Q8F213	Q8f213 leptospira	323	170.5	9.3	894	5	Q9VKG1	Q9vkg1 dirosophila
251	180.5	9.9	977	10	Q7XN51	Q7xn51 oryza sativ	324	170.5	9.3	1016	10	Q81RPT	Q81rpt1 arabidopsis
252	180	9.8	288	11	Q8BR15	Q8br15 mus musculu	325	170.5	9.3	1143	10	Q8SUD9	Q8sud9 arabidopsis
253	180	9.8	497	10	Q7XKC0	Q7xkc0 oryza sativ	326	170	9.3	376	4	Q81V47	Q81v47 homo sapien
254	180	9.8	613	10	Q940E8	Q940e8 zea mays (m	327	170	9.3	512	11	Q9CQ76	Q9cq76 mus musculu
255	179.5	9.8	530	11	Q80WQ1	Q80wq1 mus musculu	328	170	9.3	583	11	Q8BM77	Q8bm77 mus musculu
256	179.5	9.8	1102	16	Q8KC98	Q8kc98 chlorobium	329	170	9.3	631	17	Q8TN14	Q8tn14 methanosarc
257	179	9.8	428	4	Q14498	Q14498 homo sapien	330	169.5	9.3	408	16	Q8F212	Q8f212 leptospira
258	179	9.8	463	11	Q8CTV9	Q8ctv9 mus musculu	331	169.5	9.3	623	5	Q9S521	Q9s521 dirosophila
259	179	9.8	496	10	Q8GWY1	Q8gwy1 arabidopsis	332	169.5	9.3	893	10	Q9SWE6	Q9swe6 hordeum vul
260	179	9.8	933	5	Q9BDJ5	Q9bdj5 strongyloce	333	169.5	9.3	1012	10	Q7XPT3	Q7xpt3 oryza sativ
261	179	9.8	1172	10	Q9FMM3	Q9fmm3 oryza sativ	334	169.5	9.3	1130	10	Q8SB68	Q8sb68 oryza sativ
262	179	9.8	1175	10	Q7XDK0	Q7xdk0 oryza sativ	335	169.5	9.3	1130	10	Q7XGPA	Q7xgpa oryza sativ
263	179	9.8	1410	5	Q20204	Q20204 caenornabdi	336	169	9.2	437	13	Q9DE05	Q9deg5 gallus galli
264	178.5	9.8	1257	5	Q9VXR8	Q9vkr8 dirosophila	337	169	9.2	893	10	Q8LKR3	Q8lkr3 glycine max
265	178	9.7	734	11	Q35930	Q35930 mus musculu	338	169	9.2	964	10	Q8VY77	Q8vy77 arabidopsis
266	178	9.7	966	10	Q9LNX3	Q9lnx3 arabidopsis	339	169	9.2	964	10	Q9LTY3	Q9lty3 arabidopsis
267	178	9.7	1007	5	Q8MCU9	Q8mcu9 aedes aegy	340	168.5	9.2	1030	10	Q8H037	Q8h037 oryza sativ
268	177.5	9.7	537	10	Q9C769	Q9c769 arabidopsis	341	168	9.2	395	10	Q9ZT98	Q9zt98 arabidopsis
269	177.5	9.7	428	16	Q8F3F8	Q8f3f8 leptospira	342	168	9.2	510	6	Q9B9Y6	Q9by6 macaca fasc
270	177	9.7	428	16	Q8F3F8	Q8f3f8 leptospira	343	168	9.2	753	4	Q9NRR6	Q9nrr6 homo sapien
271	177	9.7	562	10	Q9MTW9	Q9mtw9 arabidopsis	344	167.5	9.2	510	5	Q9N1R8	Q9n1r8 dictyosteli
272	177	9.7	692	4	Q86YC3	Q86yc3 homo sapien	345	167	9.1	423	4	Q8ND46	Q8nd46 homo sapien
273	177	9.7	727	6	Q8HXC8	Q8hxc8 macaca fasc	346	167	9.1	483	5	Q9S5P1	Q9s5p1 dirosophila
274	176.5	9.7	353	13	Q7SY88	Q7sy88 xenopus lae	347	167	9.1	533	5	Q9VHV3	Q9vhv3 dirosophila
275	176.5	9.7	369	11	Q7TWM3	Q7twm3 mus musculu	348	167	9.1	603	5	Q22075	Q22075 caenornabdi
276	176.5	9.7	594	10	Q91WQ2	Q91wq2 arabidopsis	349	167	9.1	664	13	Q7ZT81	Q7zt81 oncorhynch
277	176.5	9.7	1112	10	Q41397	Q41397 lycopersico	350	167	9.1	693	4	Q7Z3D0	Q7z3d0 homo sapien
278	176.5	9.7	1112	10	Q41398	Q41398 lycopersico	351	167	9.1	855	10	Q9Z583	Q9z583 lycopersico
279	176	9.6	653	5	Q02329	Q02329 caenornabdi	352	167	9.1	892	10	Q84WPI	Q84wpi arabidopsis
280	176	9.6	864	10	Q8LP64	Q8lp64 arabidopsis	353	167	9.1	893	10	Q8LNS8	Q8lns8 arabidopsis
281	176	9.6	864	10	Q9T033	Q9t033 arabidopsis	354	167	9.1	1013	10	Q8LQ10	Q8lq10 oryza sativ
282	176	9.6	1048	10	Q8VYQ5	Q8vyq5 arabidopsis	355	167	9.1	1095	13	Q90XG4	Q90xg4 gallus galli
283	176	9.6	1200	5	Q860S7	Q860s7 dirosophila	356	166.5	9.1	213	6	Q865R9	Q865r9 sus scrofa
284	176	9.6	1271	11	Q8VT44	Q8vt44 mus musculu	357	166.5	9.1	606	10	Q8H609	Q8h609 oryza sativ
285	176	9.6	1271	11	Q931Z8	Q931z8 mus musculu	358	166.5	9.1	967	10	Q9LZV7	Q9lzv7 arabidopsis
286	175.5	9.6	452	16	Q8F1L8	Q8f1l8 leptospira	359	166.5	9.1	1008	10	Q8LXZ6	Q8lxz6 glycine max
287	175.5	9.6	506	10	Q9F9J3	Q9f9j3 arabidopsis	360	166.5	9.1	1274	10	Q8L155	Q8l155 oryza sativ
288	175	9.6	721	4	Q9NUV1	Q9nuv1 homo sapien	361	166.5	9.1	1274	10	Q9Z879	Q9z879 lycopersico
289	175	9.6	865	10	Q50022	Q50022 lycopersico	362	166	9.1	865	10	Q9LXZ4	Q9lxz4 glycine max
290	175	9.6	1369	4	Q60346	Q60346 homo sapien	363	166	9.1	1012	10	Q8N6Y2	Q8n6y2 homo sapien
291	175	9.6	1696	11	Q9WTR8	Q9wtr8 ratius norv	364	165.5	9.1	441	4	Q8N6Y2	Q8n6y2 homo sapien
292	174	9.5	370	13	Q9D5R4	Q9d5r4 oreochromis	365	165.5	9.1	647	5	Q86NM5	Q86nm5 dirosophila
293	174	9.5	378	11	Q8CAZ9	Q8caz9 mus musculu	366	165.5	9.1	650	5	Q9V3X1	Q9v3x1 dirosophila
294	174	9.5	462	10	Q9SUH6	Q9suh6 arabidopsis	367	165.5	9.1	825	5	Q96M63	Q96m63 homo sapien
295	174	9.5	1205	5	Q86Q70	Q86q70 dirosophila	368	165	9.0	215	11	Q91VH8	Q91vh8 mus musculu
296	173.5	9.5	441	4	Q86UN2	Q86un2 homo sapien	369	165	9.0	607	10	Q9LS89	Q9ls89 arabidopsis
297	173.5	9.5	646	11	Q8BJH4	Q8bjh4 mus musculu	370	165	9.0	783	13	Q90XG2	Q90xg2 gallus galli
298	173.5	9.5	840	11	Q8C110	Q8c110 mus musculu	371	165	9.0	789	6	Q9BE71	Q9be71 macaca fasc
299	173	9.5	404	11	Q7TP21	Q7tp21 mus musculu	372	165	9.0	832	4	Q9UTM4	Q9utm4 homo sapien
300	173	9.5	494	5	Q9VEK6	Q9vek6 dirosophila	373	165	9.0	950	13	Q90Z44	Q90z44 gallus galli
301	173	9.5	527	5	Q86P35	Q86p35 dirosophila	374	165	9.0	1143	10	Q9ZP89	Q9zp89 arabidopsis
302	173	9.5	641	5	Q8MQM0	Q8mqm0 dirosophila	375	165	9.0	1174	10	Q7XTP4	Q7xtp4 oryza sativ
303	173	9.5	915	5	Q9WZ67	Q9wz67 dirosophila	376	165	9.0	1535	5	Q23991	Q23991 dirosophila
304	173	9.5	1318	11	Q8CHE4	Q8che4 mus musculu	377	164.5	9.0	425	10	Q9FK66	Q9fk66 arabidopsis
305	172.5	9.4	404	11	Q9SZ09	Q9sz09 arabidopsis	378	164.5	9.0	426	11	Q8BOA4	Q8bqa4 mus musculu
306	172	9.4	376	11	Q8BNJ3	Q8bnj3 mus musculu	379	164.5	9.0	469	5	Q9W128	Q9w128 dirosophila
307	172	9.4	1034	10	Q7XKS4	Q7xks4 oryza sativ	380	164.5	9.0	549	10	Q9SVW8	Q9svw8 arabidopsis
308	171.5	9.4	443	11	Q9CXD9	Q9cxd9 mus musculu	381	164.5	9.0	656	5	Q19312	Q19312 caenornabdi



382	164.5	9.0	853	11	Q8GCR9	Q8GCR9 mus musculus	455	157	8.6	626	11	Q921U9	Q921U9 mus musculus
383	164.5	9.0	966	10	Q9GGL5	Q9GGL5 arabidopsis	456	157	8.6	732	5	Q8MRP3	Q8MRP3 drosophila
384	164.5	9.0	966	10	Q8GYN29	Q8GYN29 arabidopsis	457	157	8.6	862	10	Q50020	Q50020 lycopersico
385	164.5	9.0	1178	10	Q942T3	Q942T3 oryza sativ	458	157	8.6	938	10	Q91VB3	Q91VB3 arabidopsis
386	164	9.0	420	4	Q13641	Q13641 homo sapien	459	157	8.6	1025	10	Q40640	Q40640 oryza sativ
387	164	9.0	737	10	Q85700	Q85700 oryza sativ	460	157	8.6	1110	10	Q941N2	Q941N2 oryza sativ
388	164	9.0	740	10	Q49325	Q49325 arabidopsis	461	156.5	8.6	457	5	Q960D1	Q960D1 drosophila
389	164	9.0	950	4	Q95804	Q95804 homo sapien	462	156.5	8.6	646	16	Q8PDD3	Q8PDD3 xanthomonas
390	164	9.0	1109	10	Q8H4U0	Q8H4U0 oryza sativ	463	156.5	8.6	863	10	Q40235	Q40235 lycopersico
391	163.5	8.9	426	11	Q90YD9	Q90YD9 ratius norv	464	156.5	8.6	1053	10	Q94G61	Q94G61 lycopersico
392	163.5	8.9	620	11	Q8XZN9	Q8XZN9 talstonia s	465	156.5	8.6	1527	5	Q94ZV4	Q94ZV4 drosophila
393	163.5	8.9	833	11	Q80TC9	Q80TC9 mus musculus	466	156	8.5	399	5	Q8STX6	Q8STX6 encephalito
394	163	8.9	635	5	Q93539	Q93539 caenorhabdi	467	156	8.5	837	6	Q8SPR8	Q8SPR8 gorilla gor
395	163	8.9	655	5	Q50028	Q50028 lycopersico	468	156	8.5	853	10	Q8RWC6	Q8RWC6 arabidopsis
396	163	8.9	1035	11	Q92166	Q92166 mus musculus	469	156	8.5	1344	10	Q9SK94	Q9SK94 oryza sativ
397	163	8.9	1135	10	Q8W0A8	Q8W0A8 oryza sativ	470	155.5	8.5	180	11	Q8BPJ0	Q8BPJ0 mus musculus
398	163	8.9	2271	3	Q9C443	Q9C443 cryplococcu	471	155.5	8.5	371	10	Q9A1N5	Q9A1N5 oryza sativ
399	162.5	8.9	426	11	Q920L0	Q920L0 mus musculus	472	155.5	8.5	371	10	Q7XKC9	Q7XKC9 oryza sativ
400	162.5	8.9	581	11	Q9D5O5	Q9D5O5 mus musculus	473	155.5	8.5	505	10	Q7XK44	Q7XK44 oryza sativ
401	162.5	8.9	674	4	Q8WVA2	Q8WVA2 homo sapien	474	155.5	8.5	788	11	Q9CYK3	Q9CYK3 mus musculus
402	162.5	8.9	1600	10	Q9SM84	Q9SM84 oryza sativ	475	155.5	8.5	998	10	Q8LJ19	Q8LJ19 oryza sativ
403	162	8.9	581	2	Q9AN90	Q9AN90 bradyrhizob	476	155.5	8.5	1015	10	Q949G9	Q949G9 malus flori
404	162	8.9	585	16	Q89TJ5	Q89TJ5 bradyrhizob	477	155.5	8.5	1053	10	Q94G62	Q94G62 lycopersico
405	162	8.9	585	6	Q8SQH3	Q8SQH3 canis famli	478	155	8.5	590	11	Q8P2F4	Q8P2F4 mus musculus
406	162	8.9	865	10	Q50023	Q50023 lycopersico	479	155	8.5	685	16	Q8F1V0	Q8F1V0 mus musculus
407	162	8.9	964	10	Q94JU3	Q94JU3 oryza sativ	480	155	8.5	753	10	Q8SB69	Q8SB69 homo sapien
408	162	8.9	1010	10	Q8H3W8	Q8H3W8 oryza sativ	481	155	8.5	1155	10	Q8SB69	Q8SB69 oryza sativ
409	162	8.9	1100	5	Q24622	Q24622 drosophila	482	155	8.5	1155	10	Q7XK35	Q7XK35 oryza sativ
410	162	8.9	1278	10	Q9AV65	Q9AV65 oryza sativ	483	155	8.5	1155	10	Q7XK35	Q7XK35 oryza sativ
411	162	8.9	1278	10	Q7XDK3	Q7XDK3 oryza sativ	484	155	8.5	1343	10	Q7XK35	Q7XK35 oryza sativ
412	162	8.9	1420	10	Q9XE13	Q9XE13 oryza sativ	485	155	8.5	2155	3	Q9HEP4	Q9HEP4 blumeria gr
413	161.5	8.8	243	11	Q8CEB3	Q8CEB3 mus musculus	486	154.5	8.5	394	10	Q8WE39	Q8WE39 oryza sativ
414	161.5	8.8	417	6	Q8H2E1	Q8H2E1 canis famli	487	154.5	8.5	394	10	Q7XK49	Q7XK49 oryza sativ
415	161.5	8.8	866	10	Q50021	Q50021 lycopersico	488	154.5	8.5	535	10	Q9AV64	Q9AV64 oryza sativ
416	161.5	8.8	945	13	Q801F9	Q801F9 carassius a	489	154.5	8.5	535	10	Q7XDK2	Q7XDK2 oryza sativ
417	161	8.8	589	10	Q9FHL8	Q9FHL8 arabidopsis	490	154.5	8.5	976	10	Q42371	Q42371 arabidopsis
418	160.5	8.8	1181	13	Q7Z235	Q7Z235 brachydantio	491	154.5	8.5	1630	4	Q8MWV8	Q8MWV8 homo sapien
419	160	8.8	440	4	Q9H5Y7	Q9H5Y7 homo sapien	492	154.5	8.5	1630	4	Q14160	Q14160 homo sapien
420	160	8.8	528	5	Q01764	Q01764 caenorhabdi	493	154.5	8.5	1665	11	Q8V1I1	Q8V1I1 mus musculus
421	160	8.8	1134	10	Q65510	Q65510 arabidopsis	494	154.5	8.5	1694	11	Q80U72	Q80U72 mus musculus
422	160	8.8	1866	4	Q86W13	Q86W13 homo sapien	495	154.5	8.5	2309	3	Q8WZV3	Q8WZV3 neurospora
423	159.5	8.7	494	10	Q9AXA4	Q9AXA4 oryza sativ	496	154	8.4	471	5	Q9VBR3	Q9VBR3 drosophila
424	159.5	8.7	558	5	Q8MP66	Q8MP66 caenorhabdi	497	154	8.4	720	10	Q9SPB9	Q9SPB9 arabidopsis
425	159.5	8.7	559	5	Q22875	Q22875 caenorhabdi	498	154	8.4	720	10	Q80809	Q80809 arabidopsis
426	159.5	8.7	1124	5	Q8WQ08	Q8WQ08 aedes aegypt	499	154	8.4	720	10	Q9SPB8	Q9SPB8 arabidopsis
427	159.5	8.7	1140	10	Q9LR04	Q9LR04 arabidopsis	500	154	8.4	890	10	Q48849	Q48849 arabidopsis
428	159	8.7	493	11	Q80ZD7	Q80ZD7 ratius norv							
429	159	8.7	507	5	Q9N3F2	Q9N3F2 caenorhabdi							
430	159	8.7	720	10	Q50027	Q50027 lycopersico							
431	159	8.7	810	5	Q8T3J2	Q8T3J2 drosophila							
432	159	8.7	811	5	Q9VK54	Q9VK54 drosophila							
433	159	8.7	820	11	Q9D5S7	Q9D5S7 mus musculus							
434	159	8.7	880	5	P91643	P91643 drosophila							
435	159	8.7	999	10	Q82432	Q82432 malus domes							
436	158.5	8.7	478	10	Q9FW48	Q9FW48 arabidopsis							
437	158.5	8.7	480	10	Q48705	Q48705 arabidopsis							
438	158.5	8.7	493	4	Q81W71	Q81W71 homo sapien							
439	158.5	8.7	493	4	Q86WK6	Q86WK6 homo sapien							
440	158.5	8.7	792	13	Q90243	Q90243 gallus galli							
441	158.5	8.7	809	10	Q9Z0H2	Q9Z0H2 arabidopsis							
442	158.5	8.7	839	6	Q8M1Q2	Q8M1Q2 cryctolagus							
443	158.5	8.7	843	13	Q7ZRG5	Q7ZRG5 gallus galli							
444	158.5	8.7	862	10	Q50026	Q50026 lycopersico							
445	158.5	8.7	938	10	Q84XU7	Q84XU7 elaeis guin							
446	158.5	8.7	994	10	Q85B35	Q85B35 oryza sativ							
447	158	8.6	768	10	Q9Z581	Q9Z581 lycopersico							
448	157.5	8.6	325	4	Q8NAB7	Q8NAB7 homo sapien							
449	157.5	8.6	464	10	Q8W4Q3	Q8W4Q3 arabidopsis							
450	157.5	8.6	828	6	Q8SPB9	Q8SPB9 pongo pygma							
451	157	8.6	332	10	Q8GT95	Q8GT95 oryza sativ							
452	157	8.6	492	11	Q80ZD8	Q80ZD8 mus musculus							
453	157	8.6	540	5	Q9NKA4	Q9NKA4 drosophila							
454	157	8.6	550	5	Q9VUD8	Q9VUD8 drosophila							

## ALIGNMENTS

## RESULT 1

ID Q8WUA8 PRELIMINARY; PRT; 353 AA.

AC Q8WUA8; 01-MAR-2002 (TREMBLrel. 20, Created)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 NCBI\_Taxid=9606;  
 [1]  
 SEQUENCE FROM N.A.  
 RC Tissue=Colon;  
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
 RN 12  
 RP SEQUENCE FROM N.A.  
 RA Kainda N., Chen X., Rolfs A., Halleck A., Hines J., Eisenstein S.,  
 Kainda N., Raphael J., Moreira D., Kelley T., Labaer J., Lin Y.,  
 Phelan M., Farmer A.;



QY 126 ESTSSPLSDVNSHNOLEVSASATTTSSQGRALHVDLSHNLRLVHPTRAGIPART 185  
 DB 145 EFTSSPLSDINSHNRLEVSISAFTHSQGRALHVDLSHNLRLHPARASIPART 204  
 QY 186 IQLNLAMNRLHVAVNPRLDPLRYSLSDGNPLAVIGPAGAGLGLTTHLSLALORLPEL 245  
 DB 205 IQLNLAMNRLHVAVNPRLDPLRYSLSDGNPLAVIPAGAGLGLTTHLSLALORLPEL 264  
 QY 246 APGFRRLPGLQVLDLSGNPKLWAGAEVPSGLSLQELDLSGTNLVPLPEALLHLPL 305  
 DB 265 PPGFRRLPGLQVLDLSGNPKLWAGAEVPSGLSLQELDLSGTNLVPLPEALLHLPL 324  
 QY 306 QSVSVGDVRCRLVREGTYPRRPGSSPKVPLHCVDRBSAARGPTL 353  
 DB 325 QSVSVGDVRCRLVREGTYPRRPGSSPKVPLHCVDRBSAARGPTL 372

## RESULT 4

Q9UG10 PRELIMINARY; PRT; 242 AA.

AC Q9UG10; 01-MAY-2000 (Tremblrel. 13, Created)  
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
 DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)  
 DE Hypothetical protein (Fragment).  
 GN DKFZP586E011.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Uterus;  
 RA Koehrer K., Beyer A., Mewes H.W., Gassenhuber J., Wiemann S.;  
 RL Submitted (Aug-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AL10276; CABS3711.1; -  
 DR PIR; T14791; T14791.  
 DR InterPro; IPR001611; LRR.  
 DR Pfam; PF00560; LRR; 3.  
 DR Hypothetical protein.  
 FT NON\_TER  
 SQ SEQUENCE 242 AA; 25835 MW; 66CS1DB722ACECA2 CRC64;

Query Match 67.6%; Score 1235; DB 4; Length 242;  
 Best Local Similarity 99.6%; Pred. No. 2,4e-87;  
 Matches 241; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 112 SLDSHNGLTALPESPTSSPLSDVNSHNOLEVSASATTTSSQGRALHVDLSHNLRL 171  
 DB 1 SLDSHNGLTALPESPTSSPLSDVNSHNOLEVSASATTTSSQGRALHVDLSHNLRL 60  
 QY 172 LVHPTRAGIPARTIQLNLAMNRLHVAVNPRLDPLRYSLSDGNPLAVIGPAGAGLGL 231  
 DB 61 LVHPTRAGIPARTIQLNLAMNRLHVAVNPRLDPLRYSLSDGNPLAVIGPAGAGLGL 120  
 QY 232 THLSLALORLPELAPGFRRLPGLQVLDLSGNPKLWAGAEVPSGLSLQELDLSGTNL 291  
 DB 121 THLSLALORLPELAPGFRRLPGLQVLDLSGNPKLWAGAEVPSGLSLQELDLSGTNL 180  
 QY 292 VPLPEALLHLPLALQSVSVGDVRCRLVREGTYPRRPGSSPKVPLHCVDRBSAARGPT 351  
 DB 181 VPLPEALLHLPLALQSVSVGDVRCRLVREGTYPRRPGSSPKVPLHCVDRBSAARGPT 240  
 QY 352 IL 353  
 DB 241 IL 242

## RESULT 5

Q7ZUT1 PRELIMINARY; PRT; 347 AA.  
 ID Q7ZUT1;  
 AC Q7ZUT1;

DT 01-JUN-2003 (Tremblrel. 24, Created)  
 DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)  
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
 DE Hypothetical protein.  
 OS Brachydanio rerio (Zebrafish) (Danio rerio).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;  
 CC Cyprinidae; Danio.  
 OX NCBI\_TaxID=7955;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Body;  
 RA Strausberg R.;  
 RL Submitted (Mar-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC047843; AAH47843.1; -  
 DR InterPro; IPR001611; LRR.  
 DR InterPro; IPR003591; LRR\_Typ.  
 DR Pfam; PF00560; LRR; 6.  
 DR PRINTS; PR00019; LEURICRPT.  
 DR SMART; SM00366; LRR\_PS; 4.  
 DR SMART; SM00369; LRR\_Typ; 6.  
 DR Hypothetical protein.  
 SQ SEQUENCE 347 AA; 37775 MW; 1EB5446DD0871B80 CRC64;

Query Match 42.0%; Score 767; DB 13; Length 347;  
 Best Local Similarity 49.6%; Pred. No. 4.7e-51;  
 Matches 168; Conservative 48; Mismatches 109; Indels 14; Gaps 5;

QY 6 LLLAVASGQTRRCFCGCEVEVTFGLPDSFLTRVDCSGLGHMPVPIPLDTAHL 65  
 DB 11 LLGLALGCA--VKNCHQRCREVEVTFGLPDSFLTKDCSRIGGNRPVPIPLDTSHLD 68  
 QY 66 SSNRLMENVESVLAPGTYTLAGLDSHNLTSISPAFRSLRYLBSLDSHNGLTPLA 125  
 DB 69 SLNSTTSSIDTMLSGLPGTYTTLVSLDLSNNIAQISPAFRSLRYLBSLDSHNGLTPLA 128  
 QY 126 ESTSSPLSDVNSHNOLEVSASATTTSSQGRALHVDLSHNLRLVHPTRAGI 181  
 DB 129 GCFGLPFLVELDLSNQKEFNLDLFTTRQDPLIMVDSLRLTSLFRRTPGHPL 184  
 QY 182 PAPTIQSLNLMNRLHVAVNPRLDPLRYSLSDGNPLAVIGPAGAGLGLTTHLSLALOR 241  
 DB 185 --YKSLMLAGNGLKTVPKLNGIPQYLNMDGNLSSITGAFDSLTBLVHLSLSGLSE 241  
 QY 242 LPELAPGFRRLPGLQVLDLSGNPKLWAGAEVPSGLSLQELDLSGTNLVPLPEALLHL 301  
 DB 242 LTLHPGAFRSLKVLQALDLSNNSQLKTLNPNVPSGLVSLQELNLSNTAVTPLSRVFMQ 301  
 QY 302 LPALQSVSVGDVRCRLVREGTYPRRPG--SSPKVPLHC 339  
 DB 302 MPNIKSTLGPVHGWKTHMGQGFHROIQGAKPNDILTC 340

## RESULT 6

Q8N182 PRELIMINARY; PRT; 713 AA.

ID Q8N182  
 AC Q8N182; 01-OCT-2002 (Tremblrel. 22, Created)  
 DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)  
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
 DE Glioma amplified on chromosome 1 protein (leucine-rich).  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RA Strausberg R.;  
 RL Submitted (Jul-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC034047; AAH34047.1; -  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; Ig-like.

DR InterPro: IPR003598; IG\_c2.  
 DR InterPro: IPR001611; LRR.  
 DR InterPro: IPR000483; LRR\_Cterm.  
 DR InterPro: IPR003591; LRR\_Typ.  
 DR Pfam: PF00047; IG; 1.  
 DR Pfam: PF00560; LRR; 8.  
 DR Pfam: PF01463; LRRCT; 1.  
 DR PRINTS: PR00019; LEURICHRPT.  
 DR SMART: SM00409; IG; 1.  
 DR SMART: SM00408; IGc2; 1.  
 DR SMART: SM00835; IG\_LIKE; 1.  
 DR PROSITE: PS50835; IG\_LIKE; 1.  
 DR KEGG: Immunoglobulin domain.  
 DR SEQUENCE 713 AA; 78856 MW; 12A7768CFA8E1D32 CRC64;

Query Match 17.0%; Score 311.5; DB 4; Length 713;  
 Best Local Similarity 27.4%; Pred. No. 1.6e-15;  
 Matches 114; Conservative 54; Mismatches 163; Indels 85; Gaps 11;

6 LLLLAAGCAQT-----RCPFGCCCEVEYFGLPDSF--SLTRYDCSGLGPHINPVP 56  
 8 LLLAVAGATRAVVPVPMHPCPCQACQIRPWTPRSSYREATTVDGNDLFLTAVPPAL 67  
 57 PLDTAHLDTSSNRLEWNEVSLAGPGY-TTLAGLDTSHNLTSTISPTAESRLRYLSLDL 115  
 68 PAGQTLLTQNSIVRVDQSEL---GYLANLTEDLSQNSFSDARDCDFALPOLSLHL 124  
 116 SHNGLTALPAEFTS--SLSPDVLNHNQLEVSVAFTTHSGGRALHVDLSHNLIRHLP 174  
 125 EENQTLTLEDSHFGSLASLQELYNHNQLEIRAPRAGSGSLNLRH--LNSLIRAI-- 180  
 175 HPTFAGLPAPTQSLNLAHRLAV-----PNLRDL----- 205  
 181 -DSHFEMLPMLITLMIGKNKVDAILDMNFRPLANLISLVLAGMNLREISDYALEGLQSL 239  
 206 -----PLRYSLDGNPLAVPGAFAGLGGTTHLSLASLORP 243  
 240 EGSFYNDQARVRRALBOVPLKFDLKNGLQRYGPGDFANMLHKLGLANNEELV 299  
 244 ELAPSGREPLGLOVLDLQGNPKLMWAGAEVFGSLQSLQELDSTNLVLPPEALLHLP 303  
 300 SIDKFAVLNPELTKLDTNNPRLSFTHPRFHLPMETMLMNNALSAHQQTAEPL 359  
 304 ALQSVV-GQDVRGRRLVR-----EGTPRRPGSPKPYPLHCVDTRE 344  
 360 NLQVGLHGNPIRCDVIRMANATGTVRFLTPQSLCAEPDQLPRAVEVPRE 415

## RESULT 7

Q9ESY6 PRELIMINARY; PRT; 707 AA.  
 AC Q9ESY6;  
 DT 01-MAR-2001 (TREMblrel. 16, Created)  
 DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)  
 DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)  
 DE Neuronal leucine-rich repeat protein-3.  
 GN NLR3.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OC NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley;  
 RX MEDLINE=21433505; PubMed=11549284;  
 RA Fukumachi K., Matsuo Y., Kitahara C., Kuchino Y., Tsuda H.;  
 RT "Rat neuronal leucine-rich repeat protein-3: cloning and regulation of  
 the gene expression."  
 RL Biochem. Biophys. Res. Commun. 287:257-263(2001).  
 DR EMBL: AF291437; AAC00604.1; -.  
 DR PIR: JC7763; JC7763.  
 DR InterPro: IPR003961; FN\_III.  
 DR InterPro: IPR007110; IG\_LIKE.  
 DR InterPro: IPR003598; IG\_c2.

DR InterPro: IPR001611; LRR.  
 DR InterPro: IPR000483; LRR\_Cterm.  
 DR InterPro: IPR000372; LRR\_Nterm.  
 DR InterPro: IPR003591; LRR\_Typ.  
 DR Pfam: PF00041; fn3; 1.  
 DR Pfam: PF00047; IG; 1.  
 DR Pfam: PF00560; LRR; 9.  
 DR Pfam: PF01463; LRRCT; 1.  
 DR PRINTS: PR00019; LEURICHRPT.  
 DR SMART: SM00060; FN3; 1.  
 DR SMART: SM00408; IGc2; 1.  
 DR SMART: SM00082; LRRCT; 1.  
 DR SMART: SM00013; LRRNT; 1.  
 DR SMART: SM00369; LRR\_TYP; 1.  
 DR PROSITE: PS50835; IG\_LIKE; 1.  
 DR KEGG: Immunoglobulin domain.  
 DR SEQUENCE 707 AA; 79064 MW; 26A210F671EDA875 CRC64;

Query Match 14.4%; Score 263; DB 11; Length 707;  
 Best Local Similarity 25.9%; Pred. No. 8.9e-12;  
 Matches 98; Conservative 59; Mismatches 154; Indels 68; Gaps 11;

24 CCEVEYFGLPDSFSL--TRVDCSGLGPHINPVPPLDTAHLDTSSNRLEWNEVSLAGP 81  
 33 CTCEIRPWTPRSSYREATTVDGNDLGNFPARLPADQILLQTNINARIEST---D 89  
 82 GYTLTAGLDTSHNLTSTISPTAESRLRYLSLDTSHNGLTALPAES-FTSSPLSDVLN 140  
 90 FPNVLTGLDLSQNNLSVAINVQKMSQLSYLEENKLTLPKFCVGLSLQGLYVNH 149  
 141 NQLEVSVAFTTHSGGRALVD-----LSNRLHRL----- 172  
 150 NLSAISPGAFGLHNLRLHNSNRLOMINSKWEALPNLEIMLGNPIIRIKDMNQ 209  
 173 -----VHPTFAGLPAPTQSLNLAHRLAVENL--RDLPRYSL 212  
 210 PLIKRSLVIAINLTVPDDALVGI--ENLESIFYNRLNKVQVALQKAVLKFDL 267  
 213 DGNPLAVIPGAPAGLGGTTHLSLASLORLPELAPSGREPLGLOVLDLQGNPKLMWAG 272  
 268 NKNPINRIRGRDPSNMLHKLGINNPELVIDSLAVNDLPDLKRIEATNPRLSIHP 327  
 273 EVFSGLSLQELDSTNLVLPPEALLHLPLOSVV-GQDVRGRRLVR-----EGTPR 327  
 328 NAFRLPKLESIMLSNLSALYHGHTESLPKLKESISHNPICDCVIRIMNKTNR 387  
 328 --RPGSSPYPLHCVDTRE 344  
 388 FMEPDS-----LFCVDPPE 401

## RESULT 8

P97860 PRELIMINARY; PRT; 707 AA.  
 AC P97860;  
 DT 01-MAY-1997 (TREMblrel. 03, Created)  
 DT 01-MAY-1997 (TREMblrel. 03, Last sequence update)  
 DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)  
 DE Leucine-rich repeat protein precursor (Fragment).  
 GN LRRN3.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=96233817; PubMed=9011764;  
 RA Taniguchi H., Tohyama M., Takagi T.;  
 RT "Cloning and expression of a novel gene for a protein with leucine-  
 rich repeats in the developing mouse nervous system."  
 RL Brain Res. Mol. Brain Res. 36:45-52(1996).  
 DR EMBL: D49802; BA08622.1; -.  
 DR MGI: 106036; Lrrn3.

DR InterPro: IPR003961; FN III.  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003598; Ig\_c2.  
 DR InterPro: IPR001611; LRR.  
 DR InterPro: IPR000483; LRR\_Cterm.  
 DR InterPro: IPR000372; LRR\_Nterm.  
 DR InterPro: IPR003591; LRR\_Typ.  
 DR Pfam: PF00041; fn3; 1.  
 DR Pfam: PF00047; Ig; 1.  
 DR Pfam: PF00560; LRR; 10.  
 DR Pfam: PF01463; LRRCT; 1.  
 DR PRINTS: PR00019; LEURICHRPT.  
 DR SMART: SM00060; FN3; 1.  
 DR SMART: SM00408; IGC2; 1.  
 DR SMART: SM00082; LRRCT; 1.  
 DR SMART: SM00013; LRRNT; 1.  
 DR SMART: SM00369; LRR\_Typ; 1.  
 DR PROSITE: PS50835; Ig\_Like; 1.  
 DR Immunoglobulin domain; signal.  
 KM SIGNAL 1 20 POTENTIAL.  
 FT CHAIN 21 >707 POTENTIAL.  
 FT NON\_TER 707 707  
 SQ SEQUENCE 707 AA; 79156 MW; P4E7C1573DD165B CRC64;

Query Match 14.3%; Score 261; DB 11; Length 707;  
 Best Local Similarity 25.9%; Pred. No. 1.3e-11;  
 Matches 98; Conservative 59; Mismatches 154; Indels 68; Gaps 11;

QY 24 CQCEVETFGLEFDSFSL--TRVDSGLGPHIMPVPIPLDTAHLDLSNRLEMNVESTIAGP 81  
 DB 33 CTCEIRPWFPTPRSIYMEASTVDCNDLGLNFPALPADTQILLOQTNNIARIHST--D 89  
 QY 82 GYTLTAGLDLSHNLTSISPTAFRLRYESLDLSHNGLTALPAES--FTSSPLSDVNLSH 140  
 DB 90 FPNVNLGDLDSQNNLSVNTINVOKMSQLSVLEENKLTPEKLYGSLNQLVYVNH 149  
 QY 141 NQLEEVSAFTTHSQGRALHVD-----LSHNLHRL----- 172  
 DB 150 NLSSTISPGAFIGLHNLRLHLNSNRLQMINSQWFDALPNLEILMGDNPPIRIKDMNQ 209  
 QY 173 -----VPHPTAGLPAPTIQSINLNMNLHVAENL---RDLPRLRYSL 212  
 DB 210 PLVKLRSIVAGINLVEIPDDALGL--ENLSISFYDNRLSKVPQVALOKAVNLKFDL 267  
 QY 213 DGNPLAVIGPAPAGLGLTHTLSIASLQRLPELAPSGFRELPGLQVLDLSGNPKLWAGA 272  
 DB 268 NKNPINRIRRGDFSNMLHKELGINNMPELVISLAVDNLPLDKIEATNPRLSYIHP 327  
 QY 273 EVFSGLSLQELDSGTNLVLPPEALLHLPALQSVV--QDVRCRLVR---EGTYPR 327  
 DB 328 NAFPLPLKESIMLNTNALSLALYHGTIESLPNLKEISHSNPIRCDCVIRIMNKTNIR 387  
 QY 328 --RPGSSPKVPLHCVDTRE 344  
 DB 388 FMEPDS-----LFCVDPPE 401

## RESULT 9

O8CB6 PRELIMINARY; PRT; 707 AA.  
 AC O8CB6;  
 DT 01-MAR-2003 (Tremblrel. 23, Created)  
 DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)  
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
 DE Leucine rich repeat protein 3.  
 GN LRN3.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 CX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;

RX MEDLINE=22354683; PubMed=1246851;  
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 AT 60,770 full-length cDNAs."  
 RL Nature 420:563-573(2002).  
 DR EMBL: AK036316; BAC29381.1; -  
 DR MGI:106036; Lrrn3.  
 DR InterPro: IPR003961; FN III.  
 DR InterPro: IPR003599; Ig\_c2.  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003598; Ig\_c2.  
 DR InterPro: IPR001611; LRR.  
 DR InterPro: IPR000483; LRR\_Cterm.  
 DR InterPro: IPR000372; LRR\_Nterm.  
 DR InterPro: IPR003591; LRR\_Typ.  
 DR Pfam: PF00041; fn3; 1.  
 DR Pfam: PF00047; Ig; 1.  
 DR Pfam: PF00560; LRR; 10.  
 DR Pfam: PF01463; LRRCT; 1.  
 DR PRINTS: PR00019; LEURICHRPT.  
 DR SMART: SM00408; IGC2; 1.  
 DR SMART: SM00082; LRRCT; 1.  
 DR SMART: SM00013; LRRNT; 1.  
 DR PROSITE: PS50835; Ig\_Like; 1.  
 SQ SEQUENCE 707 AA; 79175 MW; DFGA009A2553E0FC CRC64;

Query Match 14.3%; Score 261; DB 11; Length 707;  
 Best Local Similarity 25.9%; Pred. No. 1.3e-11;  
 Matches 98; Conservative 59; Mismatches 154; Indels 68; Gaps 11;

QY 24 CQCEVETFGLEFDSFSL--TRVDSGLGPHIMPVPIPLDTAHLDLSNRLEMNVESTIAGP 81  
 DB 33 CTCEIRPWFPTPRSIYMEASTVDCNDLGLNFPALPADTQILLOQTNNIARIHST--D 89  
 QY 82 GYTLTAGLDLSHNLTSISPTAFRLRYESLDLSHNGLTALPAES--FTSSPLSDVNLSH 140  
 DB 90 FPNVNLGDLDSQNNLSVNTINVOKMSQLSVLEENKLTPEKLYGSLNQLVYVNH 149  
 QY 141 NQLEEVSAFTTHSQGRALHVD-----LSHNLHRL----- 172  
 DB 150 NLSSTISPGAFIGLHNLRLHLNSNRLQMINSQWFDALPNLEILMGDNPPIRIKDMNQ 209  
 QY 173 -----VPHPTAGLPAPTIQSINLNMNLHVAENL---RDLPRLRYSL 212  
 DB 210 PLVKLRSIVAGINLVEIPDDALGL--ENLSISFYDNRLSKVPQVALOKAVNLKFDL 267  
 QY 213 DGNPLAVIGPAPAGLGLTHTLSIASLQRLPELAPSGFRELPGLQVLDLSGNPKLWAGA 272  
 DB 268 NKNPINRIRRGDFSNMLHKELGINNMPELVISLAVDNLPLDKIEATNPRLSYIHP 327  
 QY 273 EVFSGLSLQELDSGTNLVLPPEALLHLPALQSVV--QDVRCRLVR---EGTYPR 327  
 DB 328 NAFPLPLKESIMLNTNALSLALYHGTIESLPNLKEISHSNPIRCDCVIRIMNKTNIR 387  
 QY 328 --RPGSSPKVPLHCVDTRE 344  
 DB 388 FMEPDS-----LFCVDPPE 401

## RESULT 10

O8CB7 PRELIMINARY; PRT; 363 AA.  
 AC O8CB7;  
 DT 01-MAR-2003 (Tremblrel. 23, Created)  
 DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)  
 DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)  
 DE G protein-coupled receptor 49.  
 GN GPR49.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Head;  
 RA MEDLINE=22354683; PubMed=12466851;  
 RX The FANTOM Consortium,  
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs."  
 RL Nature 420:563-573(2002).  
 DR EMBL; AK047873; BAC3180.1; -  
 DR MGI; MGI:1341817; Gpr49.  
 DR InterPro; IPR001611; LRR.  
 DR InterPro; IPR000372; LRR\_Nterm.  
 DR InterPro; IPR003591; LRR\_cyp.  
 DR Pfam; PF00560; LRR\_9.  
 DR Pfam; PF01462; LRRNT\_1.  
 DR PRINTS; PRO0019; LEURICHRPT.  
 DR SMART; SM00013; LRRNT\_1.  
 SQ SEQUENCE 363 AA; 39880 MW; D5E2FC449FCE2C0 CRC64;  
 Query Match 14.1%; Score 258; DB 11; Length 363;  
 Best Local Similarity 29.8%; Pred. No. 8.9e-12; Indels 66; Gaps 9;  
 Matches 89; Conservative 40; Mismatches 104;  
 OY 6 LLLAVSGAQ-----TTRPCPPGQCCEVEFPGLPDSFSLTEVDSGLGPHIMPVPIPLDT 60  
 DB 15 LLOVVAAGSSPGPAIPRGCPSHCHCEL-----DGRVLKAVDSGLSLPGLSVFT 68  
 OY 61 AHDLSRRLMEVNEVIAAGPYTTIAGLDLSHNLISISTASRLRYLESIDLINGL 120  
 DB 69 SYLLSNMNIISQLPASLL-----HRCFLKEXRLAAGNAL 102  
 OY 121 TALPAESFTS-SPLSDVNLSHNOLREVSFAFTTHSGRALHVDLSHNLHRLVPHPTRA 179  
 DB 103 THIRKATGLHSLKVLMLQNNQRLQVPEELQLNRLSLQSLRLDANH--ISYVPS---- 156  
 OY 180 GLPAPPTIOSLNLAMNRLHAVNLDLPRLRYSLDGNPLAVIGPAFAGLGGELTHLSLST 239  
 DB 157 -----CFSGHLHS-----LRHMLDNDALTDVPVOAFSLSLAQMTLA-L 195  
 OY 240 QRLPELAPSGFRELPGLOVLDLSGNPKLWAGAEVFGSLSLQELSGTNLVLPLPAL 298  
 DB 196 NKIHIALDYAFGNLSLVVLHLHNN-RHSLGKKCFDGLHSLFTLDLANNLDEFPYAI 253  
 RESULT 11  
 O9H3W5 PRELIMINARY; PRT; 708 AA.  
 AC O9H3W5; O43377;  
 DT 01-MAR-2001 (Tremblrel. 16, Created)  
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)  
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
 DE Hypothetical protein (Neuronal leucine-rich repeat protein-3)  
 DE (Leucine-rich repeat protein).  
 GN DKFZP761K2424 OR NLR-3.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Amygdala;  
 RA Bloecher H., Boecher M., Brandt P., Mewes H.W., Weill B., Wiemann S.;  
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 DT 01-NOV-1996 (Tremblrel. 01, Created)  
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)  
 DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)  
 DE TARTAN protein precursor.  
 GN TRN OR G011280.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 DT Jin L., Yu L., Zhao S.Y.;

RT "Cloning of a new human cDNA homologous to Mus musculus leucine-rich  
 RT repeat protein.";  
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AL442092; CAC09450.1; -  
 DR EMBL; AB060967; BAB47184.1; -  
 DR EMBL; AF134481; AAP97258.1; -  
 DR Genew; HGNC:117200; LRRN3.  
 DR InterPro; IPR003961; FN\_III.  
 DR InterPro; IPR007110; Ig\_IIk.  
 DR InterPro; IPR003598; Ig\_c2.  
 DR InterPro; IPR001611; LRR.  
 DR InterPro; IPR000483; LRR\_Cterm.  
 DR InterPro; IPR000372; LRR\_Nterm.  
 DR InterPro; IPR003591; LRR\_cyp.  
 DR Pfam; PF00041; fn3\_1.  
 DR Pfam; PF00047; Ig\_1.  
 DR Pfam; PF00560; LRR\_9.  
 DR Pfam; PF01463; LRRCT\_1.  
 DR Pfam; PF01462; LRRNT\_1.  
 DR PRINTS; PRO0019; LEURICHRPT.  
 DR SMART; SM00060; FN3\_1.  
 DR SMART; SM00408; Ig\_c2\_1.  
 DR SMART; SM00082; LRRCT\_1.  
 DR SMART; SM00013; LRRNT\_1.  
 DR SMART; SM00369; LRR\_TTP\_1.  
 DR PROSITE; PS50835; IG\_LIKE\_1.  
 DR Hypothetical protein; Immunoglobulin domain.  
 KM  
 SQ SEQUENCE 708 AA; 79424 MW; 24710478DEB124D1 CRC64;  
 Query Match 13.9%; Score 254; DB 4; Length 708;  
 Best Local Similarity 25.1%; Pred. No. 4.4e-11; Indels 82; Gaps 13;  
 Matches 97; Conservative 63; Mismatches 144;  
 OY 24 CCEVEFTGLPDSFSL-----TRVDSGLGPHIMPVPIPLTAHLDLSNRLEMVNEVIA 79  
 DB 33 CTEIRPW--FPRSLYMEASTVDCNDGLTFEPALPANTQILLQTNNAKIE----- 85  
 OY 80 GPGYTT-----LAGLDLSHNLISPTAFSLRYLESIDLINGLTALPASSFTS-SPL 133  
 DB 86 ---YSTDFPVNLTGLDLSQNNLSSVTINVKKPOLLSYLEENKLTPEKCLSLSNL 142  
 OY 134 SDVNLSHNOLREVSFAFTTHSGRALHYD-----LSHNLIR 171  
 DB 143 QEYINAMNLSTISPAFGLHNLRLHLSNRLOINSKWFDALPNEIIMIGEPIIR 202  
 OY 172 L-------VHPTRAGLPAPTIOGLNLAMNRLHAVNLT--RDL 205  
 DB 203 IKDMNFKPLINLRLSLVIAGINLLEIPDNLAVGL--ENLESISFYDRLTKVPHVALQKV 260  
 OY 206 PLRYSLDGNPLAVIGPAFAGLGLTHLSLQELPELAPSGFRELPGLOVLDLSGNP 265  
 DB 261 NLFFLDLKNKPIRLIRGDFSNMLKELGINNMPETLISIDSLAVDNLDPDKIKETANNP 320  
 OY 266 KLMWAGAEVFGSLSLQELDLSGTNLVPLPEALLHLPLAQSVV-GQDVRGRRLVR-- 321  
 DB 321 RLRYHPNAPFRLPKLESIMNSNLSALYHGHTESLPMLEKHSINPISNPDVIRBMN 380  
 OY 322 -EGTYPR--RPGSSPKVPLHCVDTRE 344  
 DB 381 MKKTIRFMEPDS-----LFCVDPPE 401  
 RESULT 12  
 O24250 PRELIMINARY; PRT; 733 AA.  
 AC O24250;  
 DT 01-NOV-1996 (Tremblrel. 01, Created)  
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)  
 DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)  
 DE TARTAN protein precursor.  
 GN TRN OR G011280.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

RC STAIN=Berkeley;  
RX MEDLINE=20196006; PubMed=10731132;  
RA Adams D.J., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Adamatsides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sturgeon G., Wortman J.R., Vandal M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.-H.C., Blaise R.G., Champe M., Pfeiffer B.D.,  
RA Wan X.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
RA Abril J.F., Aghayani A., An H.-J., Andrews-Peltonch C., Baldwin D.,  
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Basley E.M.,  
RA Benson K.Y., Bemis P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Borkova D., Botchan M.R., Bouck H., Brokstein P., Brothier P.,  
RA Buttle K.C., Busam D.A., Butler H., Cadenau E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA Deodson K., Doup I.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Dublin K.J., Evangelista C.C., Ferriz C., Ferreira S., Fleischmann W.,  
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glodok A., Gong P., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibgwym C.,  
RA Jaitani M., Kalusi F., Kaepen G.H., Ke Z., Kemnison U.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Laeko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Mekulov G., Mishina N.V., Moharry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nusken D.R., Pectel J.M.,  
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Port V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shie B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,  
RA Williams S.M., Woodage T., Wolley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye Y., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhu Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu Q., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,  
RT "the genome sequence of *Drosophila melanogaster*,"  
RL Science 287:2185-2195(2000).  
[2]  
RN  
RP SEQUENCE FROM N.A.  
RC STAIN=Berkeley;  
RA Stapleton M., Brokstein P., Hong L., Aghayani A., Carlson J.,  
RA Champe M., Chavez C., Dorsett V., Farfan D., Flise E., George R.,  
RA Gonzalez M., Guatin H., Li P., Liao G., Miranda A., Mungall C.J.,  
RA Nuno J., Pectel J., Paragas V., Park S., Phouenavong S., Wan X.,  
RA Yu C., Lewis S.E., Rubin G.M., Celniker S.,  
RL Submitted (Aug-2001) to the EMBL/Genbank/DBJ databases.  
DR EMBL; AE003439; AA949839.1; -  
DR EMBL; AY051439; AAX92863.1; -  
DR FLYbase; FBgn0010452; crn.  
DR InterPro; IPR001611; LRR.  
DR InterPro; IPR000463; LRR\_Cterm.  
DR InterPro; IPR000372; LRR\_Nterm.  
DR InterPro; IPR003591; LRR\_TYP.  
DR Pfam; PF01463; LRRCT; 1.  
DR Pfam; PF00560; LRR; 10.  
DR PRINTS; PR00019; LEURICHRPT.  
DR SMART; SM00082; LRRCT; 1.  
DR SMART; SM00013; LRRWT; 1.  
DR SMART; SM00369; LRR\_TYP; 2.  
SQ SEQUENCE 737 AA; 81906 MW; BE646B0149343D6 CAC64;  
Query Match 13.9%; Score 254; DB 5; Length 737;  
Best Local Similarity 27.5%; Pred. No. 4.7e-11;  
Matches 87; Conservative 46; Mismatches 135; Indels 48; Gaps 9  
QY  
DB 13 WCILASIGVEPAAGLANCPGGQCDNDTL-----VVOGEGSQLDVLPAALNPSTOR 63  
63 IDLSNRLEWVNESVLAGPGYTLAAGLIDLSHNLTSISPTAFSRRLRYDESIDLSHNGTLTA 122



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OM protein - protein search, using sw model

Run on: August 2, 2004, 16:02:32 ; Search time 54 Seconds

(Without alignments)  
1847.024 Million cell updates/sec

Title: US-10-017-390A-397  
Perfect score: 1828  
Sequence: 1 MPWPLILLAVSGAQTTRPC.....KVPILHCVDTRSNARGPITL 353

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 500 summaries

Database : A\_Geneseq\_29Jan04:\*  
1: geneseqp1980s:\*  
2: geneseqp1950s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1828	100.0	353	3 AAB24026	AAB24026 Human PRO
2	1828	100.0	353	3 AAY99455	AAY99455 Human PRO
3	1828	100.0	353	4 AAB66204	AAB66204 Proteinf o
4	1828	100.0	353	6 ABO33697	ABO33697 Novel hum
5	1828	100.0	353	7 ABO44550	ABO44550 Human sec
6	1828	100.0	353	7 ABO33574	ABO33574 Novel hum
7	1828	100.0	353	7 ADC18266	ADC18266 Human PRO
8	1828	100.0	353	7 ADD70912	ADD70912 Human sec
9	1828	100.0	353	7 ADD39989	ADD39989 Human sec
10	1828	100.0	353	7 ADD70435	ADD70435 Human sec
11	1828	100.0	353	7 ADD38556	ADD38556 Human sec
12	1828	100.0	353	7 ADD38512	ADD38512 Human sec
13	1828	100.0	353	7 ADD39035	ADD39035 Human sec
14	1828	100.0	353	7 ADD40466	ADD40466 Human sec
15	1828	100.0	353	7 ADE50687	ADE50687 Human sec
16	1828	100.0	353	7 ADE20299	ADE20299 Human sec
17	1828	100.0	353	7 ADE50210	ADE50210 Human sec
18	1828	100.0	353	7 ADE21768	ADE21768 Human sec
19	1820	99.6	353	4 AAE03427	AAE03427 Human gen
20	1820	99.6	353	4 AAU00472	AAU00472 Human TAN
21	1820	99.6	353	4 AAB88413	AAB88413 Human mem
22	1820	99.6	353	5 AAB63353	AAB63353 Human alb
23	1820	99.6	353	5 ABO32588	ABO32588 Secreted
24	1815	99.3	353	7 ADD18811	ADD18811 Human dis
25	1813	99.2	353	4 AAE03459	AAE03459 Human gen

26	1813	99.2	353	5 AAB63352	AAB63352 Human alb
27	1813	99.2	353	5 ABB97270	ABB97270 Novel hum
28	1798	95.1	337	6 ABO32590	ABO32590 Secreted
29	1636	89.5	321	7 ADB64350	ADB64350 Human pro
30	1623.5	88.8	357	3 ABA40712	ABA40712 Human ORF
31	1048	57.3	200	6 ABO32591	ABO32591 Secreted
32	578	31.6	114	6 ABO32593	ABO32593 Secreted
33	318.5	17.4	713	2 AAY13385	AAY13385 Amino aci
34	318.5	17.4	713	3 ADC78857	ADC78857 Human PRO
35	318.5	17.4	713	4 AAB80253	AAB80253 Human PRO
36	318.5	17.4	713	6 AAB71631	AAB71631 Human PRO
37	318.5	17.4	713	6 ABB71486	ABB71486 Human PRO
38	318.5	17.4	713	6 ABB71332	ABB71332 Human sec
39	318.5	17.4	713	6 ABO01815	ABO01815 Novel hum
40	318.5	17.4	713	6 ABB54388	ABB54388 Human sec
41	318.5	17.4	713	6 ABO47403	ABO47403 Human sec
42	318.5	17.4	713	6 ABB64540	ABB64540 Human sec
43	318.5	17.4	713	6 ABB67386	ABB67386 Human sec
44	318.5	17.4	713	6 ABO14806	ABO14806 Human sec
45	318.5	17.4	713	6 ABB69663	ABB69663 Novel hum
46	318.5	17.4	713	6 ABO14845	ABO14845 Human sec
47	318.5	17.4	713	6 ADE29450	ADE29450 Human sec
48	318.5	17.4	713	6 ABB62147	ABB62147 Tumour-as
49	318.5	17.4	713	6 ADA18306	ADA18306 Human sec
50	318.5	17.4	713	6 ABO32797	ABO32797 Human sec
51	318.5	17.4	713	6 ABO34857	ABO34857 Human PRO
52	318.5	17.4	713	6 ADA16281	ADA16281 Human sec
53	318.5	17.4	713	6 ADA42426	ADA42426 Human sec
54	318.5	17.4	713	6 ABO17535	ABO17535 Human PRO
55	318.5	17.4	713	7 ADA16705	ADA16705 Human sec
56	318.5	17.4	713	7 ADA13134	ADA13134 Human sec
57	318.5	17.4	713	7 ADA42002	ADA42002 Human sec
58	318.5	17.4	713	7 ADA17349	ADA17349 Human sec
59	318.5	17.4	713	7 ADA42852	ADA42852 Human sec
60	318.5	17.4	713	7 ABO17596	ABO17596 Human PRO
61	318.5	17.4	713	7 ADB77771	ADB77771 Human sec
62	318.5	17.4	713	7 ADB74907	ADB74907 Human sec
63	318.5	17.4	713	7 ADC28553	ADC28553 Human sec
64	318.5	17.4	713	7 ADC39753	ADC39753 Human sec
65	318.5	17.4	713	7 ADC40267	ADC40267 Human sec
66	318.5	17.4	713	7 ADC19091	ADC19091 Human sec
67	318.5	17.4	713	7 ADC34391	ADC34391 Human sec
68	318.5	17.4	713	7 ADC29446	ADC29446 Human sec
69	318.5	17.4	713	7 ADC28977	ADC28977 Human sec
70	318.5	17.4	713	7 ADC40862	ADC40862 Human sec
71	318.5	17.4	713	7 ADC19519	ADC19519 Human sec
72	318.5	17.4	713	7 ADC3367	ADC3367 Human sec
73	318.5	17.4	713	7 ADC13037	ADC13037 Human sec
74	318.5	17.4	713	7 ADC12489	ADC12489 Human sec
75	318.5	17.4	713	7 ADD05044	ADD05044 Human sec
76	318.5	17.4	713	7 ADD04050	ADD04050 Human sec
77	318.5	17.4	713	7 ADD03626	ADD03626 Human sec
78	318.5	17.4	713	7 ADE34878	ADE34878 Human sec
79	318.5	17.4	713	7 ADE48131	ADE48131 TAT292. 1
80	318.5	17.4	713	8 ADE79747	ADE79747 Human sec
81	318.5	17.4	713	8 ADE73423	ADE73423 Human sec
82	318.5	17.4	713	8 ADE73958	ADE73958 Human sec
83	318.5	17.4	713	6 AAE37179	AAE37179 Human LRR
84	313.5	17.1	713	6 AAE37466	AAE37466 Human GNC
85	313.5	17.1	713	7 ADE50346	ADE50346 Novel pro
86	313.5	17.1	713	7 ADE08516	ADE08516 Novel pro
87	229	15.3	700	4 ABB11787	ABB11787 Human gnt
88	229	15.3	734	6 ABR41678	ABR41678 Human DIT
89	276	15.1	883	7 ADB80464	ADB80464 Ovarian c
90	273.5	15.0	423	5 AAU91336	AAU91336 Human nov
91	269.5	14.7	490	7 ADE08146	ADE08146 Novel pro
92	267.5	14.6	611	3 AAB56643	AAB56643 Membrane-
93	267.5	14.6	672	6 ADA57213	ADA57213 Human sec
94	267.5	14.6	672	6 ADA41092	ADA41092 Human sec
95	267.5	14.6	672	6 ABR47923	ABR47923 Human sec
96	267.5	14.6	673	3 AAB38323	AAB38323 Human sec
97	267.5	14.6	673	3 AAB07428	AAB07428 Amino aci
98	267.5	14.6	673	4 AAB84689	AAB84689 Amino aci

99	267.5	14.6	673	4	AAB87533	Aab87533	Human	PRO	172	267.5	14.6	673	7	ADDD07351	Addd07351	Novel	hum
100	267.5	14.6	673	4	AAB65166	Aab65166	Human	PRO	173	267.5	14.6	673	7	ADDC82242	Adcc82242	Human	PRO
101	267.5	14.6	673	5	Aau75266	Aau75266	Human	SLI	174	267.5	14.6	673	7	ADDD08422	Addd08422	Novel	hum
102	267.5	14.6	673	5	ABG95858	Abg95858	Human	sec	175	267.5	14.6	673	7	ADDD06671	Addd06671	Novel	hum
103	267.5	14.6	673	5	ABG78042	Abg78042	Human	leu	176	267.5	14.6	673	7	ADDC82918	Adcc82918	Human	PRO
104	267.5	14.6	673	6	ABU57981	Abu57981	Human	PRO	177	267.5	14.6	673	7	ADDD55025	Addd55025	Human	PRO
105	267.5	14.6	673	6	ABU59059	Abu59059	Novel	hum	178	267.5	14.6	673	7	ADDD36020	Addd36020	Novel	hum
106	267.5	14.6	673	6	ABU82571	Abu82571	Human	sec	179	267.5	14.6	673	7	ADDD55983	Addd55983	Human	PRO
107	267.5	14.6	673	6	ABU60490	Abu60490	Human	sec	180	267.5	14.6	673	7	ADDD54421	Addd54421	Novel	hum
108	267.5	14.6	673	6	ABU73872	Abu73872	Human	PRO	181	267.5	14.6	673	7	ADDE26575	Adde26575	Novel	hum
109	267.5	14.6	673	6	ABU72457	Abu72457	Novel	hum	182	267.5	14.6	673	8	ADDE60042	Adde60042	Novel	hum
110	267.5	14.6	673	6	ABU90883	Abu90883	Novel	hum	183	267.5	14.6	673	8	ADDC52154	Adcc52154	Novel	hum
111	267.5	14.6	673	6	ABO33942	Abos33942	Human	sec	184	267.5	14.6	673	3	AAB38400	Aab38400	Fragment	
112	267.5	14.6	673	6	ABU71959	Abu71959	Novel	hum	185	266.5	14.6	673	7	ADDB55589	Adbb55589	Novel	hum
113	267.5	14.6	673	6	ABU71513	Abu71513	Human	sec	186	266.5	14.6	673	7	ADDB58506	Adbb58506	Human	sec
114	267.5	14.6	673	6	ABU72294	Abu72294	Human	PRO	187	265.5	14.5	692	2	AAU93340	Aau93340	Human	nov
115	267.5	14.6	673	6	ABU90967	Abu90967	Human	PRO	188	265	14.5	692	2	AAW93890	Aaw93890	Human	HG3
116	267.5	14.6	673	6	ABU59206	Abu59206	Human	sec	189	265	14.5	907	3	AAW93889	Aaw93889	Human	HG3
117	267.5	14.6	673	6	ABO55903	Abos55903	Human	PRO	190	265	14.5	907	3	AAW90682	Aay90682	Human	G P
118	267.5	14.6	673	6	ABO27288	Abos27288	Human	sec	191	265	14.5	907	3	AAW90687	Aay90687	Human	mut
119	267.5	14.6	673	6	ABO24483	Abos24483	Human	sec	192	265	14.5	907	3	ABP81968	Abp81968	Human	G-P
120	267.5	14.6	673	6	ABO51153	Abos1153	Human	sec	193	265	14.5	907	7	ABO06467	Abos06467	Human	G-P
121	267.5	14.6	673	6	ABO53268	Abos3268	Novel	hum	194	265	14.5	907	7	ADCC2797	Adcc2797	Human	G P
122	267.5	14.6	673	6	ABU58912	Abu58912	Human	sec	195	265	14.5	907	7	ADCE2783	Adce2783	Human	G P
123	267.5	14.6	673	6	ABU92290	Abu92290	Novel	hum	196	265	14.5	907	7	ADCE59150	Adce59150	Human	PRO
124	267.5	14.6	673	6	ABU59355	Abu59355	Novel	hum	197	265	14.5	907	7	ADDE59153	Adde59153	Human	PRO
125	267.5	14.6	673	6	ABU98270	Abu98270	Novel	hum	198	262	14.3	949	2	AAW93904	Aaw93904	Human	ACM
126	267.5	14.6	673	6	ABU89275	Abu89275	Novel	hum	199	262	14.3	949	2	AAW93905	Aaw93905	Human	ACM
127	267.5	14.6	673	6	ABU82482	Abu82482	Novel	hum	200	262	14.3	951	2	AAW93965	Aaw93965	Human	AXO
128	267.5	14.6	673	6	ABU92121	Abu92121	Novel	hum	201	262	14.3	951	2	AAW92835	Aae2835	Human	AXO
129	267.5	14.6	673	6	ABU96446	Abu96446	Human	PRO	202	262	14.3	951	4	AAE22835	Aae22835	Human	REC
130	267.5	14.6	673	6	ABU10827	Abu10827	Human	PRO	203	262	14.3	951	4	AAE66875	Aae66875	Human	REC
131	267.5	14.6	673	6	ABU81579	Abu81579	Novel	hum	204	262	14.3	951	4	AAU32972	Aau32972	Novel	hum
132	267.5	14.6	673	6	ABU72116	Abu72116	Human	PRO	205	261	14.3	951	4	AAE03524	Aae03524	Human	sec
133	267.5	14.6	673	6	ABU88518	Abu88518	Human	sec	206	261	14.3	951	2	AAO30403	Aao30403	Human	sec
134	267.5	14.6	673	6	ABO34032	Abos4032	Human	PRO	207	256	14.0	951	5	AAE042168	Aae042168	Human	IGR
135	267.5	14.6	673	6	ADBI7073	Adbi7073	Human	tra	208	256	14.0	951	5	ABE05224	Abes05224	Protein	
136	267.5	14.6	673	6	ADA37563	Ada37563	Human	sec	209	255.5	14.0	794	4	AAE82352	Aae82352	Human	leu
137	267.5	14.6	673	6	ADA21249	Ada21249	Human	sec	210	255.5	14.0	794	4	AAE03600	Aae03600	Human	ORF
138	267.5	14.6	673	6	ABO44246	Abos44246	Human	sec	211	255.5	14.0	794	4	AAE45513	Aae45513	Human	ORF
139	267.5	14.6	673	6	ADA10036	Ada10036	Human	sec	212	254	13.9	705	4	AAW78823	Aam78823	Human	pro
140	267.5	14.6	673	6	ADA19878	Ada19878	Novel	hum	213	254	13.9	705	4	AAW13355	Aay13355	Amho	act
141	267.5	14.6	673	6	ADBI7261	Adbi7261	Human	tra	214	254	13.9	708	2	AAW70030	Aay70030	Human	pro
142	267.5	14.6	673	6	ADAI7580	Adai7580	Human	PRO	215	254	13.9	708	3	ADCT8389	Adct8389	Human	PRO
143	267.5	14.6	673	6	ADA27688	Ada27688	Human	sec	216	254	13.9	708	3	AAE80223	Aae80223	Human	PRO
144	267.5	14.6	673	6	ADA20050	Ada20050	Novel	hum	217	254	13.9	708	4	AAU12320	Aau12320	Human	PRO
145	267.5	14.6	673	6	ABO34174	Abos4174	Human	sec	218	254	13.9	708	4	AAU12320	Aau12320	Human	PRO
146	267.5	14.6	673	6	ADA34258	Ada34258	Human	sec	219	254	13.9	708	5	AAU12320	Aau12320	Human	PRO
147	267.5	14.6	673	6	ADA38493	Ada38493	Human	sec	220	254	13.9	708	5	AAU12320	Aau12320	Human	PRO
148	267.5	14.6	673	6	ADA2614	Ada2614	Human	sec	221	254	13.9	708	5	AAU12320	Aau12320	Human	PRO
149	267.5	14.6	673	6	ADA00347	Ada00347	Human	sec	222	254	13.9	708	6	ABO17661	Abos17661	Novel	hum
150	267.5	14.6	673	7	ABO53118	Abos53118	Human	sec	223	254	13.9	708	6	ABU71456	Abu71456	Human	PRO
151	267.5	14.6	673	7	ADA22175	Ada22175	Human	sec	224	254	13.9	708	6	ADAI7456	Adai7456	Human	sec
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153	267.5	14.6	673	7	ADA06341	Ada06341	Human	sec	226	254	13.9	708	6	ABU81018	Abu81018	Human	PRO
154	267.5	14.6	673	7	ADA39034	Ada39034	Human	sec	227	254	13.9	708	6	ABO01785	Abos01785	Novel	hum
155	267.5	14.6	673	7	ADA39034	Ada39034	Human	sec	228	254	13.9	708	6	ABU65718	Abu65718	Human	PRO
156	267.5	14.6	673	7	ADBB6060	Adbb6060	Human	PRO	229	254	13.9	708	6	ABU54358	Abu54358	Human	sec
157	267.5	14.6	673	7	ADBB68075	Adbb68075	Human	PRO	230	254	13.9	708	6	ADAI41222	Adai41222	LOC	92468
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167	267.5	14.6	673	7	ADBB68075	Adbb68075	Human	PRO	240	254	13.9	708	6	ADAI41222	Adai41222	LOC	92468
168	267.5	14.6	673	7	ADBB68075	Adbb68075	Human	PRO	241	254	13.9	708	6	ADAI41222	Adai41222	LOC	92468
169	267.5	14.6	673	7	ADBB68075	Adbb68075	Human	PRO	242	254	13.9	708	6	ADAI41222	Adai41222	LOC	92468
170	267.5	14.6	673	7	ADBB68075	Adbb68075	Human	PRO	243	254	13.9	708	6	ADAI41222	Adai41222	LOC	92468
171	267.5	14.6	673	7	ADBB68075	Adbb68075	Human	PRO	244	254	13.9	708	6	ADAI41222	Adai41222	LOC	92468

245	254	13.9	708	6	ADB29274	AdB29274	Human	sec	318	254	13.9	708	7	ADB38038	AdB38038	Novel	hum
246	254	13.9	708	6	ADA18898	Ada18898	Human	PRO	319	254	13.9	708	7	ADB66510	AdB66510	Novel	hum
247	254	13.9	708	6	ADA61521	Ada61521	Homo	sapi	320	254	13.9	708	7	ADB89590	AdB89590	Human	PRO
248	254	13.9	708	6	ADB19306	AdB19306	Novel	hum	321	254	13.9	708	7	ADB90322	AdB90322	Human	PRO
249	254	13.9	708	6	ADB27847	AdB27847	Human	PRO	322	254	13.9	708	7	ADB77595	AdB77595	Human	sec
250	254	13.9	708	6	ADA86326	Ada86326	Novel	hum	323	254	13.9	708	7	ADB39423	AdB39423	Novel	hum
251	254	13.9	708	6	ADB15890	AdB15890	Human	PRO	324	254	13.9	708	7	ADB74731	AdB74731	Human	sec
252	254	13.9	708	6	ADA47676	Ada47676	Human	PRO	325	254	13.9	708	7	ADB47046	AdB47046	Novel	hum
253	254	13.9	708	6	ADA18130	Ada18130	Human	sec	326	254	13.9	708	7	ADB86653	AdB86653	Human	PRO
254	254	13.9	708	6	ABO32767	AbO32767	Human	sec	327	254	13.9	708	7	ADB77258	AdB77258	Novel	hum
255	254	13.9	708	6	ADA67471	Ada67471	Human	PRO	328	254	13.9	708	7	ADB34415	AdB34415	Human	PRO
256	254	13.9	708	6	ADB30478	AdB30478	Human	PRO	329	254	13.9	708	7	ADB35519	AdB35519	Human	PRO
257	254	13.9	708	6	ADA85774	Ada85774	Novel	hum	330	254	13.9	708	7	ADB33863	AdB33863	Human	PRO
258	254	13.9	708	6	ADA96986	Ada96986	Human	PRO	331	254	13.9	708	7	ADB34967	AdB34967	Human	PRO
259	254	13.9	708	6	ADA79290	Ada79290	Human	PRO	332	254	13.9	708	7	ADB36071	AdB36071	Human	PRO
260	254	13.9	708	6	ADA87429	Ada87429	Novel	hum	333	254	13.9	708	7	ADB46466	AdB46466	Novel	hum
261	254	13.9	708	6	ADB16631	AdB16631	Human	PRO	334	254	13.9	708	7	ADC28377	AdC28377	Human	sec
262	254	13.9	708	6	ABO34827	AbO34827	Human	PRO	335	254	13.9	708	7	ADC39577	AdC39577	Human	sec
263	254	13.9	708	6	ADA16105	Ada16105	Human	sec	336	254	13.9	708	7	ADC40091	AdC40091	Human	sec
264	254	13.9	708	6	ADA91723	Ada91723	Novel	hum	337	254	13.9	708	7	ADC18919	AdC18919	Human	sec
265	254	13.9	708	6	ADB14786	AdB14786	Human	PRO	338	254	13.9	708	7	ADC34215	AdC34215	Human	sec
266	254	13.9	708	6	ADB18747	AdB18747	Novel	hum	339	254	13.9	708	7	ADC29270	AdC29270	Human	sec
267	254	13.9	708	6	ADA93962	Ada93962	Human	PRO	340	254	13.9	708	7	ADC28801	AdC28801	Human	sec
268	254	13.9	708	6	ADB19858	AdB19858	Novel	hum	341	254	13.9	708	7	ADC40686	AdC40686	Human	sec
269	254	13.9	708	6	ADB13170	AdB13170	Human	PRO	342	254	13.9	708	7	ADC19343	AdC19343	Human	sec
270	254	13.9	708	6	ABO43297	AbO43297	Novel	hum	343	254	13.9	708	7	ADC33791	AdC33791	Human	sec
271	254	13.9	708	6	ADA74424	Ada74424	Human	PRO	344	254	13.9	708	7	ADC12861	AdC12861	Human	sec
272	254	13.9	708	6	ADA42250	Ada42250	Human	sec	345	254	13.9	708	7	ADC50339	AdC50339	Novel	hum
273	254	13.9	708	6	ADB24657	AdB24657	Human	PRO	346	254	13.9	708	7	ADC71866	AdC71866	Novel	hum
274	254	13.9	708	6	ADA82181	Ada82181	Human	PRO	347	254	13.9	708	7	ADC59865	AdC59865	Novel	hum
275	254	13.9	708	6	ADA75144	Ada75144	Human	PRO	348	254	13.9	708	7	ADC52872	AdC52872	Novel	hum
276	254	13.9	708	6	ADA85222	Ada85222	Novel	hum	349	254	13.9	708	7	ADC57226	AdC57226	Novel	hum
277	254	13.9	708	6	ADA84670	Ada84670	Novel	hum	350	254	13.9	708	7	ADC60417	AdC60417	Novel	hum
278	254	13.9	708	6	ABO17505	AbO17505	Human	PRO	351	254	13.9	708	7	ADC50892	AdC50892	Novel	hum
279	254	13.9	708	6	ADB29926	AdB29926	Human	PRO	352	254	13.9	708	7	ADC65419	AdC65419	Human	PRO
280	254	13.9	708	6	ADA80454	Ada80454	Human	PRO	353	254	13.9	708	7	ADC54517	AdC54517	Novel	hum
281	254	13.9	708	6	ADA75696	Ada75696	Human	PRO	354	254	13.9	708	7	ADC53478	AdC53478	Novel	hum
282	254	13.9	708	6	ADA46921	Ada46921	Human	PRO	355	254	13.9	708	7	ADC59001	AdC59001	Novel	hum
283	254	13.9	708	6	ADB25217	AdB25217	Human	PRO	356	254	13.9	708	7	ADC55879	AdC55879	Novel	hum
284	254	13.9	708	6	ADA93393	Ada93393	Human	PRO	357	254	13.9	708	7	ADC58449	AdC58449	Novel	hum
285	254	13.9	708	6	ADB26743	AdB26743	Human	PRO	358	254	13.9	708	7	ADC12313	AdC12313	Human	sec
286	254	13.9	708	6	ADB31030	AdB31030	Human	PRO	359	254	13.9	708	7	ADDP03123	AdD03123	Human	sec
287	254	13.9	708	6	ADA60958	Ada60958	Homo	sapi	360	254	13.9	708	7	ADC90115	AdC90115	Novel	hum
288	254	13.9	708	6	ADB24105	AdB24105	Human	PRO	361	254	13.9	708	7	ADC69534	AdC69534	Human	PRO
289	254	13.9	708	6	ADA96434	Ada96434	Human	PRO	362	254	13.9	708	7	ADC48423	AdC48423	Human	PRO
290	254	13.9	708	6	ADA81006	Ada81006	Human	PRO	363	254	13.9	708	7	ADD09952	AdD09952	Human	PRO
291	254	13.9	708	6	ADA95882	Ada95882	Human	PRO	364	254	13.9	708	7	ADD04527	AdD04527	Novel	hum
292	254	13.9	708	6	ADB26191	AdB26191	Human	PRO	365	254	13.9	708	7	ADC80483	AdC80483	Novel	hum
293	254	13.9	708	6	ADB21676	AdB21676	Novel	hum	366	254	13.9	708	7	ADD10990	AdD10990	Human	PRO
294	254	13.9	708	7	ADA77455	Ada77455	Human	PRO	367	254	13.9	708	7	ADC47871	AdC47871	Human	PRO
295	254	13.9	708	7	ADB18195	AdB18195	Human	PRO	368	254	13.9	708	7	ADD04868	AdD04868	Human	sec
296	254	13.9	708	7	ADA86878	Ada86878	Novel	hum	369	254	13.9	708	7	ADC79931	AdC79931	Novel	hum
297	254	13.9	708	7	ADA16529	Ada16529	Human	sec	370	254	13.9	708	7	ADD09400	AdD09400	Human	PRO
298	254	13.9	708	7	ADA12958	Ada12958	Human	sec	371	254	13.9	708	7	ADD03874	AdD03874	Human	sec
299	254	13.9	708	7	ADA41826	Ada41826	Human	sec	372	254	13.9	708	7	ADD03450	AdD03450	Human	sec
300	254	13.9	708	7	ADA87981	Ada87981	Novel	hum	373	254	13.9	708	7	ADD41113	AdD41113	Novel	hum
301	254	13.9	708	7	ADA45369	Ada45369	Novel	hum	374	254	13.9	708	7	ADD52252	AdD52252	Human	PRO
302	254	13.9	708	7	ADA17173	Ada17173	Human	sec	375	254	13.9	708	7	ADD52992	AdD52992	Human	PRO
303	254	13.9	708	7	ADA42676	Ada42676	Human	sec	376	254	13.9	708	7	ADD53544	AdD53544	Novel	hum
304	254	13.9	708	7	ADB28399	AdB28399	Human	PRO	377	254	13.9	708	7	ADD51700	AdD51700	Human	PRO
305	254	13.9	708	7	ADB28951	AdB28951	Human	PRO	378	254	13.9	708	7	ADD02499	AdD02499	Human	PRO
306	254	13.9	708	7	ADA76903	Ada76903	Human	PRO	379	254	13.9	708	7	ADD01933	AdD01933	Human	PRO
307	254	13.9	708	7	ADA88533	Ada88533	Novel	hum	380	254	13.9	708	7	ADD54115	AdD54115	Novel	hum
308	254	13.9	708	7	ADA97538	Ada97538	Human	PRO	381	254	13.9	708	7	ADD92432	AdD92432	Human	PRO
309	254	13.9	708	7	ADB27295	AdB27295	Human	PRO	382	254	13.9	708	7	ADD91328	AdD91328	Human	PRO
310	254	13.9	708	7	ADB22228	AdB22228	Novel	hum	383	254	13.9	708	7	ADD03942	AdD03942	Human	PRO
311	254	13.9	708	7	ABO17566	AbO17566	Human	PRO	384	254	13.9	708	7	ADB32239	AdB32239	Novel	hum
312	254	13.9	708	7	ADA66919	Ada66919	Human	PRO	385	254	13.9	708	7	ADB22171	AdB22171	Human	PRO
313	254	13.9	708	7	ADB23780	AdB23780	Human	PRO	386	254	13.9	708	7	ADD79395	AdD79395	Human	PRO
314	254	13.9	708	7	ADB23553	AdB23553	Human	PRO	387	254	13.9	708	7	ADE41931	AdE41931	Human	PRO
315	254	13.9	708	7	ADA92275	Ada92275	Novel	hum	388	254	13.9	708	7	ADD17748	AdD17748	Human	PRO
316	254	13.9	708	7	ADB15338	AdB15338	Human	PRO	389	254	13.9	708	7	ADD91880	AdD91880	Human	PRO
317	254	13.9	708	7	ADB38590	AdB38590	Novel	hum	390	254	13.9	708	7	ADB33343	AdB33343	Novel	hum

391	254	13.9	708	7	AD333895	Ad333895	Novel hum
392	254	13.9	708	7	AD79947	Ad79947	Human PRO
393	254	13.9	708	7	AD92984	Ad92984	Human PRO
394	254	13.9	708	7	AD319404	Ad319404	Human PRO
395	254	13.9	708	7	AD34702	Ad34702	Human sec
396	254	13.9	708	7	AD34702	Ad34702	Human sec
397	254	13.9	708	7	AD34702	Ad34702	Human PRO
398	254	13.9	708	7	AD34702	Ad34702	Human PRO
399	254	13.9	708	7	AD34702	Ad34702	Human PRO
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401	254	13.9	708	7	AD34702	Ad34702	Human PRO
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411	254	13.9	708	7	AD34702	Ad34702	Human PRO
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455	254	13.9	708	7	AD34702	Ad34702	Human PRO
456	254	13.9	708	7	AD34702	Ad34702	Human PRO
457	254	13.9	708	7	AD34702	Ad34702	Human PRO
458	254	13.9	708	7	AD34702	Ad34702	Human PRO
459	254	13.9	708	7	AD34702	Ad34702	Human PRO
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461	254	13.9	708	7	AD34702	Ad34702	Human PRO
462	254	13.9	708	7	AD34702	Ad34702	Human PRO
463	254	13.9	708	7	AD34702	Ad34702	Human PRO

464	238.5	13.0	379	5	AB84831	Ab84831	Human PRO
465	238.5	13.0	379	5	AB85437	Ab85437	Human PRO
466	238.5	13.0	379	5	AB85920	Ab85920	Human PRO
467	238.5	13.0	379	5	AB86230	Ab86230	Human PRO
468	238.5	13.0	379	5	AB86496	Ab86496	Human PRO
469	238.5	13.0	379	5	AB86733	Ab86733	Human PRO
470	238.5	13.0	379	5	AB86835	Ab86835	Human PRO
471	238.5	13.0	379	5	AB86916	Ab86916	Human PRO
472	238.5	13.0	379	5	AB87236	Ab87236	Human PRO
473	238.5	13.0	379	5	AB87814	Ab87814	Human PRO
474	238.5	13.0	379	5	AB88004	Ab88004	Human PRO
475	238.5	13.0	379	5	AB88301	Ab88301	Human PRO
476	238.5	13.0	379	5	AB88603	Ab88603	Human PRO
477	238.5	13.0	379	5	AB88909	Ab88909	Human PRO
478	238.5	13.0	379	5	AB89102	Ab89102	Human PRO
479	238.5	13.0	379	5	AB89421	Ab89421	Human PRO
480	238.5	13.0	379	5	AB89720	Ab89720	Human PRO
481	238.5	13.0	379	5	AB90028	Ab90028	Human PRO
482	238.5	13.0	379	5	AB90327	Ab90327	Human PRO
483	238.5	13.0	379	5	AB90628	Ab90628	Human PRO
484	238.5	13.0	379	5	AB90929	Ab90929	Human PRO
485	238.5	13.0	379	5	AB91230	Ab91230	Human PRO
486	238.5	13.0	379	5	AB91531	Ab91531	Human PRO
487	238.5	13.0	379	5	AB91832	Ab91832	Human PRO
488	238.5	13.0	379	5	AB92133	Ab92133	Human PRO
489	238.5	13.0	379	5	AB92434	Ab92434	Human PRO
490	238.5	13.0	379	5	AB92735	Ab92735	Human PRO
491	238.5	13.0	379	5	AB93036	Ab93036	Human PRO
492	238.5	13.0	379	5	AB93337	Ab93337	Human PRO
493	238.5	13.0	379	5	AB93638	Ab93638	Human PRO
494	238.5	13.0	379	5	AB93939	Ab93939	Human PRO
495	238.5	13.0	379	5	AB94240	Ab94240	Human PRO
496	238.5	13.0	379	5	AB94541	Ab94541	Human PRO
497	238.5	13.0	379	5	AB94842	Ab94842	Human PRO
498	238.5	13.0	379	5	AB95143	Ab95143	Human PRO
499	238.5	13.0	379	5	AB95444	Ab95444	Human PRO
500	238.5	13.0	379	5	AB95745	Ab95745	Human PRO

## ALIGNMENTS

## RESULT 1

ID AAB24026 standard; protein: 353 AA.

AAB24026; 25-JAN-2001 (first entry)

Human PRO1788 protein sequence SEQ IDNO:18.

Human; tumour; diagnosis; neoplastic disease; proliferation; cancer; identification; tumorigenesis; anticancer; detection.

Homo sapiens.

WO200053750-A1.

14-SEP-2000.

02-DEC-1999; 99WO-US028551.

08-MAR-1999; 99WO-US005028.

01-SEP-1999; 99WO-US020111.

29-OCT-1999; 98US-0162506P.

30-NOV-1999; 98WO-US028313.

01-DEC-1999; 99WO-US028634.

(GENTH ) GENTECH INC.

Botstein D, Goddard A, Gurney AL, Roy MA, Watanabe CK, Wood WI;

XX

DR WPI; 2000-594320/56.  
DR N-PSDB; AAC58108.  
XX Antibodies specific for PRO polypeptides, used to diagnose and inhibit  
PT the growth of tumors in mammals, and to identify inhibitors of PRO  
PT polypeptide activity or expression.  
XX  
PS Claim 61; Fig 12; 226pp; English.  
XX  
CC The present invention describes an antibody that binds to a human protein  
CC (1) selected from: PRO381; PRO1269; PRO1410; PRO1755; PRO1780; PRO3444;  
CC PRO1927; PRO3567; PRO1295; PRO1293; PRO1303; PRO1344; PRO1554; PRO1397;  
CC PRO407; PRO1555; PRO1096; PRO2038; and PRO2262. (1) has anticancer  
CC activity and can be used to diagnose tumors in mammals, by detecting  
CC complex formation when the antibody is contacted with test cells.  
CC increased expression of genes encoding (1) can also be detected to  
CC diagnose tumors. Agents which inhibit the activity of (1), especially  
CC the antibodies, or an antisense oligonucleotide which hybridizes to genes  
CC encoding (1), can be used to inhibit tumour growth, preferably by  
CC inducing cell death. Methods from the present invention can be used to  
CC identify compounds which inhibit the biological activity of (1). AAC58019  
CC to AAC58102 represent PCR primers and hybridisation probes used in  
CC examples from the present invention for human PRO sequences. AAC58103 to  
CC AAC58122 and AAB24021 to AAB24040 represent human PRO polynucleotide and  
CC protein sequences given in the exemplification of the present invention  
XX  
SQ Sequence 353 AA:  
Query Match 100.0%; Score 1828; DB 3; Length 353;  
Best Local Similarity 100.0%; Pred. No. 1.5e-167;  
Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX PD 09-MAR-2000.  
XX PF 01-SEP-1999;  
XX 99WO-US020111.  
PR 01-SEP-1998; 98US-0098716P.  
PR 01-SEP-1998; 98US-0098749P.  
PR 01-SEP-1998; 98US-0098750P.  
PR 02-SEP-1998; 98US-0098803P.  
PR 02-SEP-1998; 98US-0098821P.  
PR 02-SEP-1998; 98US-0098843P.  
PR 09-SEP-1998; 98US-0099356P.  
PR 09-SEP-1998; 98US-0099398P.  
PR 09-SEP-1998; 98US-0099602P.  
PR 09-SEP-1998; 98US-0099642P.  
PR 10-SEP-1998; 98US-0099741P.  
PR 10-SEP-1998; 98US-0099754P.  
PR 10-SEP-1998; 98US-0099763P.  
PR 10-SEP-1998; 98US-0099782P.  
PR 10-SEP-1998; 98US-0099808P.  
PR 10-SEP-1998; 98US-0099812P.  
PR 10-SEP-1998; 98US-0099815P.  
PR 10-SEP-1998; 98US-0099816P.  
PR 15-SEP-1998; 98US-0100385P.  
PR 15-SEP-1998; 98US-0100388P.  
PR 15-SEP-1998; 98US-0100390P.  
PR 16-SEP-1998; 98US-0100584P.  
PR 16-SEP-1998; 98US-0100627P.  
PR 16-SEP-1998; 98US-0100661P.  
PR 16-SEP-1998; 98US-0100662P.  
PR 16-SEP-1998; 98US-0100664P.  
PR 17-SEP-1998; 98US-0100683P.  
PR 17-SEP-1998; 98US-0100684P.  
PR 17-SEP-1998; 98US-0100710P.  
PR 17-SEP-1998; 98US-0100711P.  
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RESULT 2  
AA99455  
ID AA99455 standard; protein; 353 AA.  
XX  
XX AA99455;  
XX  
XX 08-AUG-2000 (first entry)  
XX  
XX DE Human PRO1786 (UNQ850) amino acid sequence SEQ ID NO:397.  
XX  
XX KW Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;  
XX transmembrane; secretion; immunoadhesion; pharmaceutical; screening.  
XX  
XX OS Homo sapiens.  
XX  
XX FN WO200012708-A2.



XX WPI; 2001-071395/08.  
 DR Secreted and transmembrane proteins and nucleic acids designated PRO.  
 XX PT useful as hybridization probes, in chromosome and gene mapping and gene  
 PT therapy.  
 XX  
 XX Claim 1; Fig 232; 787bp; English.  
 PS  
 CC The present invention relates to secreted and transmembrane proteins.  
 CC These proteins and the DNA encoding them may be used as hybridization  
 CC probes, in chromosome and gene mapping and in the generation of anti-  
 CC sense RNA and DNA. They may also be used to generate either  
 CC transgenic animals or knockout animals which are in turn useful for  
 CC development and screening of therapeutically useful reagents. The nucleic  
 CC acids may also be used in gene therapy  
 XX  
 SO Sequence 353 AA;  
 Query Match 100.0%; Score 1828; DB 4; Length 353;  
 Best local similarity 100.0%; Pred. No. 1.5e-167;  
 Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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 Db 1 MPWPLLLLAASGAGTTRPCPGGCGEVEFGFLDFDSFLTRVDCSGLGPPIHMPYPIPLDT 60  
 Cy 61 AHDLSNRLEMVESVLAGPGYTTLAGLDLSNHLTISPTAFSRRLVLESIDLSHNGL 120  
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 Cy 181 LPAPTIQSLNANRILHVPNLRLPLRYSLSDGNPAVLGPAGAGLGTHTLSASTQ 240  
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 Cy 241 RLPEIABSGFRELPGLOYLDSGNPKLNAGAEVFGSLISQEIIDLSTNLVLPPEALL 300  
 Db 241 RLPEIABSGFRELPGLOYLDSGNPKLNAGAEVFGSLISQEIIDLSTNLVLPPEALL 300  
 Cy 301 HLPALQSVAGQDYRCRLVREGTYPRRPGSSPKVPIHCVTRRSAAAGPTIL 353  
 Db 301 HLPALQSVAGQDYRCRLVREGTYPRRPGSSPKVPIHCVTRRSAAAGPTIL 353

RESULT 4  
 ABO33697  
 ID ABO33697 standard; protein; 353 AA.  
 XX  
 AC ABO33697;  
 XX  
 DT 17-SEP-2003 (first entry)  
 XX  
 DE Novel human secreted and transmembrane protein PRO1788.  
 XX  
 KW Human; secreted and transmembrane protein; PRO; angiogenesis;  
 KW endothelial cell proliferation; wound healing; immune response;  
 KW T-lymphocytes proliferation; neonatal heart hypertrophy; tumour;  
 KW cardiac insufficiency disorder; calcium flux; inflammation;  
 KW vascular endothelial growth factor-stimulated proliferation;  
 KW mammalian kidney mesangial cell proliferation; Berger disease;  
 KW nephropathy; Schanlein-Henoch purpura; celiac disease; Cronn's disease;  
 KW dermatitis herpetiformis; diabetes; haemoglobin switch; insulinemia;  
 KW pancreatic beta-cell precursor cell differentiation; thalassemia;  
 KW obesity; auditory hair cell regeneration; hearing loss; bone disorder;  
 KW cartilage disorder; sports injury; arthritis.  
 KW Homo sapiens.  
 XX  
 OS US2003073130-A1.  
 PN

XX PD 17-APR-2003.  
 XX  
 XX 11-DEC-2001. 2001US-00015869.  
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PR 22-DEC-1998; 98US-0113296P.  
PR 30-DEC-1998; 98US-0114223P.  
PR 05-JAN-1999; 99WO-US000106.  
PR 16-APR-1999; 99US-0129674P.  
PR 23-JUN-1999; 99US-0141037P.  
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PR 26-JUL-1999; 99US-0145698P.  
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PR 02-DEC-1999; 99WO-US028551.  
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PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004342.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 02-MAR-2000; 2000WO-US005841.

PR 15-MAR-2000; 2000WO-US006884.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 10-NOV-2000; 2000WO-US030873.  
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PR 28-FEB-2001; 2001WO-US006520.  
PR 01-MAR-2001; 2001WO-US006666.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 20-JUN-2001; 2001WO-US019692.  
PR 29-JUN-2001; 2001WO-US021066.  
PR 09-JUL-2001; 2001WO-US021735.  
PR 04-SEP-2001; 2001US-00946374.  
  
XX (GETH ) GENENTECH INC.  
XX  
XX Baker KP, Botstein D, Desnoyers L, Baton DL, Ferrara N, Fong S;  
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ,  
PI Fan J, Fagan NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK,  
PI Williams EM, Wood WI;  
XX  
XX MPI; 2003-585293/55.  
DR N-PSDB; ACD68519.  
XX  
XX Novel isolated PRO polypeptides e.g. PRO1130, PRO1275, PRO1418, PRO1555,  
PT PRO1787 that modulate glucose or free fatty acid uptake by skeletal-  
PT muscle cells, and are useful for treating diabetes, hyper- or hypo-  
  
Query Match 100.0%; Score 1828; DB 6; Length 353;  
Best Local Similarity 100.0%; Pred. No. 1.5e-167;  
Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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DB 1 MPWLLILAVSGAQTTRPCPGQCEVETFGFDFDSLSLRVCSGCGHIMPVPLDT 60  
QY 61 AHDLSNRLEMNESVLAGPGYTTLAGLDSHLTLISPTAFSRRLYESLDSHNGL 120  
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RESULT 5  
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ID ABO44550 standard: protein; 353 AA.  
XX ABO44550;  
AC  
XX  
XX  
DT 01-OCT-2003 (first entry)  
XX  
DE Human secreted/transmembrane protein PRO1788.  
XX  
XX Human; secreted protein; transmembrane protein; PRO; vulnery; cardiant;  
KW antidiabetic; anorectic; antiarthritis; angiogenesis; cancer;

KM adrenal cortical capillary; endothelial cell growth; wound healing;  
KM stimulated T-lymphocyte proliferation; immune response suppression;  
KM neonatal heart hypertrophy; cardiac insufficiency disorder;  
KM vascular endothelial growth factor; inflammation; mononuclear cell;  
KM eosinophil; diabetes; obesity; or hyper-insulinaemia; hypo-insulinaemia;  
KM chondrocyte redifferentiation; bone disorder; cartilage disorder;  
KM sports injury; arthritis.  
XX  
OS Homo sapiens.  
XX  
PN US2003044841-A1.  
XX  
PD 06-MAR-2003.  
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PF 06-DEC-2001; 2001US-00006856.  
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PR 30-DEC-1998; 98US-0114423P.  
PR 05-JAN-1999; 99WO-US000106.  
PR 16-APR-1999; 99US-0129674P.  
PR 23-JUN-1999; 99US-0144137P.  
PR 20-JUL-1999; 99US-0144758P.  
PR 26-JUL-1999; 99US-0145698P.

PR 01-SEP-1999; 99MO-US020111.  
 PR 15-SEP-1999; 99MO-US021194.  
 PR 29-OCT-1999; 99US-0162506P.  
 PR 30-NOV-1999; 99MO-US028313.  
 PR 02-DEC-1999; 99MO-US028551.  
 PR 16-DEC-1999; 99MO-US030095.  
 PR 05-JAN-2000; 2000MO-US000219.  
 PR 06-JAN-2000; 2000MO-US000376.  
 PR 11-FEB-2000; 2000MO-US003565.  
 PR 18-FEB-2000; 2000MO-US004342.  
 PR 24-FEB-2000; 2000MO-US005004.  
 PR 02-MAR-2000; 2000MO-US005841.  
 PR 15-MAR-2000; 2000MO-US006884.  
 PR 17-MAY-2000; 2000MO-US013705.  
 PR 22-MAY-2000; 2000MO-US014042.  
 PR 30-MAY-2000; 2000MO-US014941.  
 PR 02-JUN-2000; 2000MO-US015264.  
 PR 23-AUG-2000; 2000MO-US023522.  
 PR 24-AUG-2000; 2000MO-US023328.  
 PR 08-NOV-2000; 2000MO-US030952.  
 PR 10-NOV-2000; 2000MO-US030873.  
 PR 01-DEC-2000; 2000MO-US032878.  
 PR 28-FEB-2001; 2001MO-US006520.  
 PR 01-MAR-2001; 2001MO-US006666.  
 PR 01-JUN-2001; 2001MO-US017800.  
 PR 20-JUN-2001; 2001MO-US019692.  
 PR 29-JUN-2001; 2001MO-US021066.  
 PR 09-JUL-2001; 2001MO-US021735.  
 PR 04-SEP-2001; 2001US-00946374.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Baker KP, Bolstein D, Desnoyers L, Baton DL, Ferrara N, Fong S;  
 PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;  
 PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;  
 PI Williams PM, Wood WI;  
 XX  
 DR WPI; 2003-492259/46.  
 DR N-PSDB; ACH04621.  
 XX  
 PT Novel secreted and transmembrane polypeptides and polynucleotides  
 PT encoding them useful for treating various cardiac insufficiencies  
 PT disorders, bone and/or cartilage disorders such as sports injuries and  
 PT arthritis.

Query Match 100.0%; Score 1828; DB 7; Length 353;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-167;  
 Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 61 AHDLSNRLNEMVESYLAGGYTTLAGDLSHNLITSPTAFSRRLYESIDLSHNGI 120  
 QY 61 AHDLSNRLNEMVESYLAGGYTTLAGDLSHNLITSPTAFSRRLYESIDLSHNGI 120  
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 QY 121 TALPASFTSSPLSDVNLSHNQREVSAFTTHSQGRALHVDLSHNLIRLVPHTPRA 180  
 DB 121 TALPASFTSSPLSDVNLSHNQREVSAFTTHSQGRALHVDLSHNLIRLVPHTPRA 180  
 QY 121 TALPASFTSSPLSDVNLSHNQREVSAFTTHSQGRALHVDLSHNLIRLVPHTPRA 180  
 DB 121 TALPASFTSSPLSDVNLSHNQREVSAFTTHSQGRALHVDLSHNLIRLVPHTPRA 180  
 QY 181 LPATTSQNLNANRLAAVNLRLDPLRYSLDGNPLAVPGPAGLGLTTHSLASQ 240  
 DB 181 LPATTSQNLNANRLAAVNLRLDPLRYSLDGNPLAVPGPAGLGLTTHSLASQ 240  
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 DB 241 RLPEIASGPRELPGLOVLDLSGNPKLNWAGAEVFSGLSLQSLDLSGTLVPLPALLI 300  
 QY 301 HLPALQSVSVQDVRGRIRVREGTPRRPGSSPVPLHCDTRESARGETIL 353  
 DB 301 HLPALQSVSVQDVRGRIRVREGTPRRPGSSPVPLHCDTRESARGETIL 353

RESULT 6  
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 ID ABO33574 standard; protein; 353 AA.  
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 AC ABO33574;  
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 DT 17-SEP-2003 (first entry)  
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 DE Novel human secreted and transmembrane protein PRO1788.  
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 KW Human; secreted and transmembrane protein; PRO; gene therapy; vaccine;  
 KM tissue typing; chromosome identification; vaccine.  
 XX  
 OS Homo sapiens.  
 XX  
 FN US2003073129-A1.  
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 PD 17-APR-2003.  
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 PF 04-SEP-2001; 2001US-00946374.  
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 PR 17-NOV-1998; 98US-0108779P.  
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 PR 18-NOV-1998; 98US-0108851P.  
 PR 18-NOV-1998; 98US-0108852P.  
 PR 18-NOV-1998; 98US-0108858P.  
 PR 18-NOV-1998; 98US-0108904P.  
 PR 22-DEC-1998; 98US-00218517.

PR 22-DEC-1998; 98US-0113296P.  
 PR 30-DEC-1998; 98US-0114223P.  
 PR 05-JAN-1999; 99MO-US000106.  
 PR 12-APR-1999; 99US-00284291.  
 PR 16-APR-1999; 99US-0129674P.  
 PR 23-JUN-1999; 99US-0141037P.  
 PR 20-JUL-1999; 99US-0144758P.  
 PR 26-JUL-1999; 99US-0145698P.  
 PR 01-SEP-1999; 99MO-US020111.  
 PR 15-SEP-1999; 99MO-US021194.  
 PR 18-OCT-1999; 99US-00403297.  
 PR 30-NOV-1999; 99MO-US028313.  
 PR 02-DEC-1999; 99MO-US028551.  
 PR 16-DEC-1999; 99MO-US030095.  
 PR 05-JAN-2000; 2000MO-US000219.  
 PR 06-JAN-2000; 2000MO-US000376.  
 PR 11-FEB-2000; 2000MO-US003565.  
 PR 18-FEB-2000; 2000MO-US004342.  
 PR 24-FEB-2000; 2000MO-US005004.  
 PR 02-MAR-2000; 2000MO-US005841.  
 PR 15-MAR-2000; 2000MO-US006884.  
 PR 17-MAY-2000; 2000MO-US013705.  
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 PR 30-MAY-2000; 2000MO-US014941.  
 PR 02-JUN-2000; 2000MO-US015264.  
 PR 23-AUG-2000; 2000MO-US023522.  
 PR 24-AUG-2000; 2000MO-US023328.  
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 PR 01-DEC-2000; 2000MO-US032678.  
 PR 28-FEB-2001; 2001MO-US006520.  
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 PR 14-JUN-2001; 2001US-00882636.  
 PR 20-JUN-2001; 2001MO-US019692.  
 PR 29-JUN-2001; 2001MO-US021066.  
 PR 09-JUL-2001; 2001MO-US021735.

## (GETH ) GENENTECH INC.

PA Baker KP, Botstein D, Desnovers L, Eason DL, Ferrara N, Fong S;  
 PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gunney AL, Hillan KJ,  
 PI Pan U, Paoni NF, Roy NA, Smith V, Stewart TA, Tumas D, Watanabe CK,  
 PI Williams PM, Wood WI;  
 XX WPI: 2003-585292/55.  
 DR N-PSDB; ACD68165.

XX Novel isolated PRO polypeptides e.g. PRO1491 and PRO1571, useful in the  
 PT preparation of a medicament for treating a condition responsive to PRO  
 PT polypeptide, and as therapeutic vaccines e.g. vaccines.  
 XX Claim 12; Fig 232; 561pp; English.

CC The invention describes an isolated PRO (secreted and transmembrane)  
 CC polypeptide (I), having at least 80% sequence identity to a sequence

Query Match 100.0%; Score 1828; DB 7; Length 353;  
 Best Local Similarity 100.0%; Pred. No. 1,56-167;  
 Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPPPLILLAVGAGQTRPCPGCCCEVETFGLPFSLTRVDCGLGPHIVPPIPT 60  
 DB 1 MPPPLILLAVGAGQTRPCPGCCCEVETFGLPFSLTRVDCGLGPHIVPPIPT 60  
 QY 61 AHLDSSNRLNEMVNSVLAPGYTTLAGLDSHNLITISIPAFSRRLRYLESLSHNG 120  
 DB 61 AHLDSSNRLNEMVNSVLAPGYTTLAGLDSHNLITISIPAFSRRLRYLESLSHNG 120  
 QY 121 TALPASFTSSPLSDVNLSHNOLREVSVSAFTTHSQRLAHVDLSHNLHRLVPHPTAG 180  
 DB 121 TALPASFTSSPLSDVNLSHNOLREVSVSAFTTHSQRLAHVDLSHNLHRLVPHPTAG 180

QY 181 LPAPTQSIINLANRRLHAVPNLRDLPLRFLSLDQNPFLAVIGGAPAGLGLTHLSIASIQ 240  
Db 181 LPAPTQSIINLANRRLHAVPNLRDLPLRFLSLDQNPFLAVIGGAPAGLGLTHLSIASIQ 240  
QY 241 RLPELAPSGPREPLGQVLDLSDGNPKLNAGAEVFSGLSLOELDSTNLVLPREALIL 300  
Db 241 RLPELAPSGPREPLGQVLDLSDGNPKLNAGAEVFSGLSLOELDSTNLVLPREALIL 300  
QY 301 HLPALQSVSYGVQDVRRCRLVRECTYPRPQSSPKVPELHCVDTRRESAARPTIL 353  
Db 301 HLPALQSVSYGVQDVRRCRLVRECTYPRPQSSPKVPELHCVDTRRESAARPTIL 353  
RESULT 7  
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XX ADCl8266;  
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DT 18-DEC-2003 (first entry)  
DE Human PRO polypeptide #116.  
XX  
XX Human; PRO; protein electrophoresis; chromosome mapping; gene mapping;  
XX genetic disorder.  
XX  
XX Homo sapiens.  
XX  
XX US2003064925-A1.  
XX  
XX 03-APR-2003.  
XX  
XX 10-DEC-2001; 2001US-00013907.  
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XX 01-SEP-1998; 98US-0098716Z.  
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PR 01-SEP-1998; 98US-0098750P.  
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PR 09-SEP-1998; 98US-0098956P.  
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 PR 23-JUN-1999; 99US-0141037P.  
 PR 26-JUL-1999; 99US-0144758P.  
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 PR 15-SEP-1999; 99WO-US021194.  
 PR 29-OCT-1999; 99US-0162506P.  
 PR 30-NOV-1999; 99WO-US028313.  
 PR 02-DEC-1999; 99WO-US028551.  
 PR 16-DEC-1999; 99WO-US030095.  
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 PR 06-JAN-2000; 2000WO-US000376.  
 PR 11-FEB-2000; 2000WO-US000356.  
 PR 18-FEB-2000; 2000WO-US000432.  
 PR 24-FEB-2000; 2000WO-US005004.  
 PR 02-MAR-2000; 2000WO-US005841.  
 PR 15-MAR-2000; 2000WO-US006884.  
 PR 17-MAY-2000; 2000WO-US013705.  
 PR 22-MAY-2000; 2000WO-US014042.  
 PR 30-MAY-2000; 2000WO-US014941.  
 PR 02-JUN-2000; 2000WO-US015264.  
 PR 23-AUG-2000; 2000WO-US023522.  
 PR 24-AUG-2000; 2000WO-US023328.  
 PR 08-NOV-2000; 2000WO-US030952.  
 PR 10-NOV-2000; 2000WO-US030873.  
 PR 01-DEC-2000; 2000WO-US032678.  
 PR 28-FEB-2001; 2001WO-US006520.  
 PR 01-MAR-2001; 2001WO-US006666.  
 PR 01-JUN-2001; 2001WO-US017800.  
 PR 20-JUN-2001; 2001WO-US019692.  
 PR 29-JUN-2001; 2001WO-US021066.  
 PR 09-JUL-2001; 2001WO-US021735.  
 PR 04-SEP-2001; 2001US-00946374.  
 XX  
 PA (GENTH ) GENENTECH INC.  
 XX  
 PI Baker KP, Botstein D, Desnoyers L, Eaton DJ, Ferrara N, Fong S;  
 PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;  
 PI Pan J, Pecht NR, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;  
 PI Williams PM, Wood WI;  
 XX  
 DR WPI; 2003-555602/52.  
 DR N-PSDB; ADC18265.  
 XX  
 PT Novel isolated PRO polypeptides e.g. PRO1491 and PRO1571, useful in the  
 PT preparation of a medicament for treating a condition responsive to PRO  
 PT polypeptide, and as therapeutic agents e.g. vaccines.  
 XX  
 PS Claim 12; SEQ ID NO 397; 555BP; English.  
 XX  
 CC The invention relates to human PRO polypeptides and the polynucleotides  
 CC encoding them. The sequences are useful in the preparation of a  
 CC medicament for treating a condition responsive to a PRO polypeptide. The  
 CC polypeptides are useful in a number of functional biological assays, as  
 CC molecular weight markers for protein electrophoresis and as therapeutic

Query Match 100.0%; Score 1828; DB 7; Length 353;  
 Best Local Similarity 100.0%; Pred. No. 1.se-167;

Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MPWLLILLIIVAGACTTTPCPGCGCEVETGGLFDSFLTRVDSGLGPHIMVPIPLDT 60  
 DB 1 MPWLLILLIIVAGACTTTPCPGCGCEVETGGLFDSFLTRVDSGLGPHIMVPIPLDT 60  
 QY 61 AMLDLSNRLEWNVNSVLAGPGYTLGLDLSHNLTLISPTAFRLRYLSLDSHNGL 120  
 DB 61 AMLDLSNRLEWNVNSVLAGPGYTLGLDLSHNLTLISPTAFRLRYLSLDSHNGL 120  
 QY 121 TALPAESFTSPSLSVNLSHNLQREVSVSAFTTHSQGRALHVDLSHNLHRLVPHTRAG 180  
 DB 121 TALPAESFTSPSLSVNLSHNLQREVSVSAFTTHSQGRALHVDLSHNLHRLVPHTRAG 180  
 QY 181 LPAPTIGSINLANNRLHAVPNIRDLPLAYTSLDGNPLAVTRGAPAGIGLTHLSLASLQ 240  
 DB 181 LPAPTIGSINLANNRLHAVPNIRDLPLAYTSLDGNPLAVTRGAPAGIGLTHLSLASLQ 240  
 QY 241 RLPETLAPSGFRELPELQVLDLSGNPKLNWAGAEVFSGLSLQELDLSGNTLVLPPEALL 300  
 DB 241 RLPETLAPSGFRELPELQVLDLSGNPKLNWAGAEVFSGLSLQELDLSGNTLVLPPEALL 300  
 QY 301 HLPALQSVSVGQDVRCRRLVREGTYPRRPGSSPKYPLHCVDTRRSANAGPTLL 353  
 DB 301 HLPALQSVSVGQDVRCRRLVREGTYPRRPGSSPKYPLHCVDTRRSANAGPTLL 353  
 RESULT 8  
 ADD70912  
 ID ADD70912 standard; protein; 353 AA.  
 AC XX  
 AC ADD70912;  
 DT XX  
 DT 15-JUN-2004 (first entry)  
 DE XX  
 DE Human secreted/transmembrane protein PRO1788.  
 DE XX  
 KW Human; secreted protein; transmembrane protein; PRO; tumour;  
 KW immune response; cardiac insufficiency disorder; calcium flux;  
 KW umbilical vein endothelial cell; bone disorder; cartilage disorder;  
 KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;  
 KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;  
 KW dermatitis; herpeticiformis; Crohn's disease; thalassemia.  
 XX  
 OS Homo sapiens.  
 OS XX  
 PN US2003099625-A1.  
 XX  
 PD 29-MAY-2003.  
 XX  
 PF 12-DEC-2001; 2001US-00015386.  
 XX  
 PR 01-SEP-1998; 98US-0098716P.  
 PR 01-SEP-1998; 98US-0098723P.  
 PR 01-SEP-1998; 98US-0098749P.  
 PR 01-SEP-1998; 98US-0098750P.  
 PR 02-SEP-1998; 98US-0098803P.  
 PR 02-SEP-1998; 98US-0098821P.  
 PR 02-SEP-1998; 98US-0098843P.  
 PR 03-SEP-1998; 98US-0098536P.  
 PR 03-SEP-1998; 98US-0098596P.  
 PR 03-SEP-1998; 98US-0098598P.  
 PR 03-SEP-1998; 98US-0098602P.  
 PR 03-SEP-1998; 98US-0098642P.  
 PR 10-SEP-1998; 98US-0098741P.  
 PR 10-SEP-1998; 98US-0098754P.  
 PR 10-SEP-1998; 98US-0098763P.  
 PR 10-SEP-1998; 98US-0098792P.  
 PR 10-SEP-1998; 98US-0098808P.  
 PR 10-SEP-1998; 98US-0098812P.  
 PR 10-SEP-1998; 98US-0098815P.  
 PR 10-SEP-1998; 98US-0098816P.  
 PR 15-SEP-1998; 98US-0100385P.

PR 15-SEP-1998; 98US-0100388P.  
PR 15-SEP-1998; 98US-0100390P.  
PR 16-SEP-1998; 98US-0100584P.  
PR 16-SEP-1998; 98US-0100627P.  
PR 16-SEP-1998; 98US-0100661P.  
PR 16-SEP-1998; 98US-0100662P.  
PR 16-SEP-1998; 98US-0100664P.  
PR 17-SEP-1998; 98US-0100683P.  
PR 17-SEP-1998; 98US-0100684P.  
PR 17-SEP-1998; 98US-0100710P.  
PR 17-SEP-1998; 98US-0100711P.  
PR 17-SEP-1998; 98US-0100919P.  
PR 17-SEP-1998; 98US-0100930P.  
PR 18-SEP-1998; 98US-0100848P.  
PR 18-SEP-1998; 98US-0100849P.  
PR 18-SEP-1998; 98US-0101014P.  
PR 18-SEP-1998; 98US-0101068P.  
PR 18-SEP-1998; 98US-0101071P.  
PR 22-SEP-1998; 98US-0101279P.  
PR 23-SEP-1998; 98US-0101471P.  
PR 23-SEP-1998; 98US-0101472P.  
PR 23-SEP-1998; 98US-0101474P.  
PR 23-SEP-1998; 98US-0101475P.  
PR 23-SEP-1998; 98US-0101476P.  
PR 23-SEP-1998; 98US-0101477P.  
PR 23-SEP-1998; 98US-0101479P.  
PR 24-SEP-1998; 98US-0101738P.  
PR 24-SEP-1998; 98US-0101741P.  
PR 24-SEP-1998; 98US-0101743P.  
PR 24-SEP-1998; 98US-0101915P.  
PR 24-SEP-1998; 98US-0101916P.  
PR 29-SEP-1998; 98US-0102207P.  
PR 29-SEP-1998; 98US-0102240P.  
PR 29-SEP-1998; 98US-0102307P.  
PR 29-SEP-1998; 98US-0102330P.  
PR 29-SEP-1998; 98US-0102331P.  
PR 30-SEP-1998; 98US-0102444P.  
PR 30-SEP-1998; 98US-0102472P.  
PR 30-SEP-1998; 98US-0102510P.  
PR 30-SEP-1998; 98US-0102511P.  
PR 01-OCT-1998; 98US-0102684P.  
PR 01-OCT-1998; 98US-0102687P.  
PR 02-OCT-1998; 98US-0102965P.  
PR 06-OCT-1998; 98US-0103288P.  
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PR 07-OCT-1998; 98US-0103314P.  
PR 07-OCT-1998; 98US-0103315P.  
PR 07-OCT-1998; 98US-0103328P.  
PR 07-OCT-1998; 98US-0103355P.  
PR 07-OCT-1998; 98US-0103366P.  
PR 07-OCT-1998; 98US-0103401P.  
PR 08-OCT-1998; 98US-0103633P.  
PR 08-OCT-1998; 98US-0103678P.  
PR 08-OCT-1998; 98US-0103679P.  
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PR 14-OCT-1998; 98US-0104257P.  
PR 20-OCT-1998; 98US-0104987P.  
PR 20-OCT-1998; 98US-0105000P.  
PR 20-OCT-1998; 98US-0105002P.  
PR 21-OCT-1998; 98US-0105104P.  
PR 22-OCT-1998; 98US-0105169P.  
PR 22-OCT-1998; 98US-0105266P.  
PR 26-OCT-1998; 98US-0105693P.  
PR 26-OCT-1998; 98US-0105694P.  
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PR 27-OCT-1998; 98US-0105881P.  
PR 27-OCT-1998; 98US-0105882P.  
PR 27-OCT-1998; 98US-0106062P.  
PR 28-OCT-1998; 98US-0106023P.  
PR 28-OCT-1998; 98US-0106029P.  
PR 28-OCT-1998; 98US-0106030P.  
PR 28-OCT-1998; 98US-0106032P.  
PR 28-OCT-1998; 98US-0106033P.  
  
PR 28-OCT-1998; 98US-0106178P.  
PR 29-OCT-1998; 98US-0106248P.  
PR 29-OCT-1998; 98US-0106348P.  
PR 29-OCT-1998; 98US-0106500P.  
PR 30-OCT-1998; 98US-0106454P.  
PR 03-NOV-1998; 98US-0106856P.  
PR 03-NOV-1998; 98US-0106902P.  
PR 03-NOV-1998; 98US-0106905P.  
PR 03-NOV-1998; 98US-0106919P.  
PR 03-NOV-1998; 98US-0106932P.  
PR 03-NOV-1998; 98US-0106934P.  
PR 10-NOV-1998; 98US-0107753P.  
PR 17-NOV-1998; 98US-0108775P.  
PR 17-NOV-1998; 98US-0108779P.  
PR 17-NOV-1998; 98US-0108787P.  
PR 17-NOV-1998; 98US-0108788P.  
PR 17-NOV-1998; 98US-0108801P.  
PR 17-NOV-1998; 98US-0108802P.  
PR 17-NOV-1998; 98US-0108806P.  
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PR 17-NOV-1998; 98US-0108877P.  
PR 17-NOV-1998; 98US-0108879P.  
PR 18-NOV-1998; 98US-0108925P.  
PR 18-NOV-1998; 98US-0108848P.  
PR 18-NOV-1998; 98US-0108849P.  
PR 18-NOV-1998; 98US-0108850P.  
PR 18-NOV-1998; 98US-0108851P.  
PR 18-NOV-1998; 98US-0108852P.  
PR 18-NOV-1998; 98US-0108858P.  
PR 18-NOV-1998; 98US-0108904P.  
PR 22-DEC-1998; 98US-0113296P.  
PR 30-DEC-1998; 98US-0114223P.  
PR 05-JAN-1999; 99WO-US000106P.  
PR 16-APR-1999; 99US-0129674P.  
PR 23-JUN-1999; 99US-0141037P.  
PR 20-JUL-1999; 99US-0144758P.  
PR 26-JUL-1999; 99US-0145688P.  
PR 01-SEP-1999; 99WO-US020111P.  
PR 15-SEP-1999; 99WO-US021194P.  
PR 29-OCT-1999; 99US-0162506P.  
PR 30-NOV-1999; 99WO-US028313P.  
PR 02-DEC-1999; 99WO-US028551P.  
PR 16-DEC-1999; 99WO-US030095P.  
PR 05-JAN-2000; 2000WO-US000219P.  
PR 06-JAN-2000; 2000WO-US000376P.  
PR 11-FEB-2000; 2000WO-US003565P.  
PR 18-FEB-2000; 2000WO-US004342P.  
PR 24-FEB-2000; 2000WO-US005004P.  
PR 02-MAR-2000; 2000WO-US005841P.  
PR 15-MAR-2000; 2000WO-US006884P.  
PR 17-MAY-2000; 2000WO-US013705P.  
PR 22-MAY-2000; 2000WO-US014042P.  
PR 30-MAY-2000; 2000WO-US014941P.  
PR 02-JUN-2000; 2000WO-US015264P.  
PR 23-AUG-2000; 2000WO-US023528P.  
PR 24-AUG-2000; 2000WO-US023528P.  
PR 08-NOV-2000; 2000WO-US030952P.  
PR 10-NOV-2000; 2000WO-US030873P.  
PR 01-DEC-2000; 2000WO-US032678P.  
PR 28-FEB-2001; 2001WO-US006650P.  
PR 01-MAR-2001; 2001WO-US006666P.  
PR 01-JUN-2001; 2001WO-US017800P.  
PR 20-JUN-2001; 2001WO-US019692P.  
PR 29-JUN-2001; 2001WO-US021066P.  
PR 09-JUL-2001; 2001WO-US021735P.  
PR 04-SEP-2001; 2001US-00946374P.  
  
(GETH ) GENENTECH INC.  
XX  
PA Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Rong S,  
XX Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ,  
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK,  
PI Williams PM, Wood WI;  
XX



DR WPI; 2003-874602/81.  
 DR N-PSDB; ADD70911.  
 XX Novel isolated PRO polypeptides e.g., PRO1130, PRO1275, PRO1418, PRO1555, PRO1787 affect glucose or free fatty acid (FFA) uptake by skeletal muscle cells and are useful for treating diabetes or hyper- or hypo-insulinemia.  
 PS Claim 12; SEQ ID NO 397; 553bp; English.  
 CC The invention relates to an isolated PRO polypeptide (secreted or

Query Match 100.0%; Score 1828; DB 7; Length 353;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-167;  
 Matches 353; Conservativity 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPWPLILLLAVSGAQTTRPCFPGCQCEVEFTGGLFDFSILTRVDCSGGLGPHIMVPIPLDT 60  
 |||||  
 Db 1 MPWPLILLLAVSGAQTTRPCFPGCQCEVEFTGGLFDFSILTRVDCSGGLGPHIMVPIPLDT 60  
 |||||  
 QY 61 AHDLSNRLKEMVNESVLAQPGYTTAGLDLSHNLTSISPTAFSRLRYESLIDLSHNGI 120  
 |||||  
 Db 61 AHDLSNRLKEMVNESVLAQPGYTTAGLDLSHNLTSISPTAFSRLRYESLIDLSHNGI 120  
 |||||  
 QY 121 TALPABESFTSPSDVLSHNLREVSAFTTHSGORALHVDLSHNLHRLVPHPTPAG 180  
 |||||  
 Db 121 TALPABESFTSPSDVLSHNLREVSAFTTHSGORALHVDLSHNLHRLVPHPTPAG 180  
 |||||  
 QY 181 LPAPTIOGLNLANRLHAVENLRDLPLRYLSDGNPLAVIPGAPAGLGGIATHSLASIQ 240  
 |||||  
 Db 181 LPAPTIOGLNLANRLHAVENLRDLPLRYLSDGNPLAVIPGAPAGLGGIATHSLASIQ 240  
 |||||  
 QY 241 RLPEPLASGREGREPLGLOVLDLSGNPKLNAGAEVFGSLSLQELIDLSGTMVLPPLALL 300  
 |||||  
 Db 241 RLPEPLASGREGREPLGLOVLDLSGNPKLNAGAEVFGSLSLQELIDLSGTMVLPPLALL 300  
 |||||  
 QY 301 HLPALQSVSGQDVRCRLVREGTYPRRPGSSPKVPFACHVDTRESAARGPTIL 353  
 |||||  
 Db 301 HLPALQSVSGQDVRCRLVREGTYPRRPGSSPKVPFACHVDTRESAARGPTIL 353  
 |||||

RESULT 9  
 ADD39989  
 ID ADD39989 standard; protein; 353 AA.  
 XX  
 AC ADD39989;  
 DT 15-JAN-2004 (first entry)  
 XX  
 DE Human secreted/transmembrane protein PRO1788.  
 XX  
 KM Human; secreted protein; transmembrane protein; PRO; tumour;  
 KM immune response; cardiac insufficiency disorder; calcium flux;  
 KM umbilical vein endothelial cell; bone disorder; cartilage disorder;  
 KM arthritis; wound healing; diabetes; skeletal muscle cells; obesity;  
 KM Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;  
 KM dermatitis; herpeticiformis; Crohn's disease; thalassemia.  
 XX  
 OS Homo sapiens.  
 PN US2003083462-A1.  
 XX  
 PD 01-MAY-2003.  
 XX  
 PF 10-DEC-2001; 2001US-00013913.  
 XX  
 PR 05-JAN-1999; 99WO-US000106.  
 PR 01-SEP-1999; 99WO-US020111.  
 PR 15-SEP-1999; 99WO-US021194.  
 PR 30-NOV-1999; 99WO-US028313.  
 PR 02-DEC-1999; 99WO-US028511.  
 PR 16-DEC-1999; 99WO-US030095.  
 PR 05-JAN-2000; 2000WO-US000219.  
 PR 06-JAN-2000; 2000WO-US000376.

PR 11-FEB-2000; 2000WO-US003565.  
 PR 18-FEB-2000; 2000WO-US004342.  
 PR 24-FEB-2000; 2000WO-US005004.  
 PR 02-MAR-2000; 2000WO-US005841.  
 PR 15-MAR-2000; 2000WO-US006884.  
 PR 17-MAY-2000; 2000WO-US013705.  
 PR 22-MAY-2000; 2000WO-US014042.  
 PR 30-MAY-2000; 2000WO-US014941.  
 PR 02-JUN-2000; 2000WO-US015264.  
 PR 23-AUG-2000; 2000WO-US023522.  
 PR 24-AUG-2000; 2000WO-US023328.  
 PR 08-NOV-2000; 2000WO-US030952.  
 PR 10-NOV-2000; 2000WO-US030873.  
 PR 01-DEC-2000; 2000WO-US032678.  
 PR 28-FEB-2001; 2001WO-US006520.  
 PR 01-MAR-2001; 2001WO-US006666.  
 PR 01-JUN-2001; 2001WO-US017800.  
 PR 20-JUN-2001; 2001WO-US019632.  
 PR 29-JUN-2001; 2001WO-US021056.  
 PR 09-JUL-2001; 2001WO-US021735.  
 PR 04-SEP-2001; 2001US-00946374.  
 XX  
 PA (GENENTECH INC.  
 XX  
 PI Baker KP, Borstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;  
 PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;  
 PI Pan J, Paoni NF, Roy NA, Smith V, Stewart TA, Tumas D, Wacanabe CK;  
 PI Williams PM, Wood WI;  
 XX  
 DR WPI; 2003-755122/71.  
 DR N-PSDB; ADD39988.  
 XX  
 PT New secreted and transmembrane PRO polypeptides useful for treating  
 PT cancers, kidney disorders, Crohn's disease, diabetes mellitus, hyper- or  
 PT hypo-insulinemia, sports injuries and arthritis.  
 XX  
 PS Claim 12; SEQ ID NO 397; 553bp; English.  
 XX

The invention relates to an isolated PRO polypeptide (secreted or transmembrane protein) having at least 80% amino acid sequence identity to an amino acid sequence chosen from 123 fully defined sequences as given in the specification (including their extracellular domains either CC or without their associated signal peptides. Also include are the CC nucleotide (NA) sequences encoding PRO, a vector comprising the PRO NA, a host cell comprising the vector, producing PRO, a chimeric molecule comprising PRO fused to a heterologous amino acid sequence, and an anti-PRO antibody. PRO is useful as molecular weight markers for protein electrophoresis and also for chromosome identification. PRO is also useful for tissue typing. PRO and PRO NA are useful as hybridisation probes for a cDNA library to isolate the full-length PRO cDNA. PRO NA is useful for generating transgenic animals or knock-out animals which are CC useful in development and screening useful reagents. PRO NA is also useful in gene therapy. PRO1244, PRO1286 and PRO1303 polypeptides are useful for treating cancers. PRO1550, PRO1418 and PRO1410 polypeptides are useful for suppressing immune response. PRO1246 polypeptide is useful for treating cardiac insufficiency disorders. PRO1561 polypeptide is also useful for treating tumours. PRO1246 and PRO1561 polypeptides are useful for stimulating calcium flux in human umbilical vein endothelial cells. PRO1265, PRO1250 and PRO1474 polypeptides are useful for treating bone and/or cartilage disorders (e.g., arthritis) and wound healing. PRO1130, PRO1275 and PRO1418 polypeptides are useful for treating diabetes in skeletal muscle cells and obesity. PRO1265, PRO1244 and PRO1382 polypeptides are useful for treating Berger disease or other nephropathies associated with Schonlein-Henoch purpura, coeliac disease, dermatitis, herpeticiformis or Crohn's disease. PRO1478, PRO1265, PRO1412, PRO1279, PRO1304, PRO1306, PRO1418, PRO1410 and PRO1575 are useful in treating thalassemias. The present sequence represents a PRO protein of the invention.

Query Match 100.0%; Score 1828; DB 7; Length 353;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-167;

Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPWLLLLAVSAQCTTRPCPCGCCCEVEETFGULFDSFSLTRVDCSGLGPHIMVPIDPT 60  
Db 1 MPWLLLLAVSAQCTTRPCPCGCCCEVEETFGULFDSFSLTRVDCSGLGPHIMVPIDPT 60

QY 61 AHLDSSNRIEMVNESVLAGPGYTTLAGIDLSHNLITSISPAFSRLRLTESLSHNL 120  
Db 61 AHLDSSNRIEMVNESVLAGPGYTTLAGIDLSHNLITSISPAFSRLRLTESLSHNL 120

QY 121 TALPASFTSPSPDLNLSHNLREVSFAFTTSSQGRALHYDLSHNLHRLVPPPTAG 180  
Db 121 TALPASFTSPSPDLNLSHNLREVSFAFTTSSQGRALHYDLSHNLHRLVPPPTAG 180

QY 181 LPAFTIQTINLAWNRLLHAYPNLRDLPLRYLSLDGNPLAVIGCAFGAGLGLTHLSLAIQ 240  
Db 181 LPAFTIQTINLAWNRLLHAYPNLRDLPLRYLSLDGNPLAVIGCAFGAGLGLTHLSLAIQ 240

QY 241 RLPELAPSGRRLPGIQTVDLSGNPKLWAGAEVFGSLQELDLSGTLNVLPEALL 300  
Db 241 RLPELAPSGRRLPGIQTVDLSGNPKLWAGAEVFGSLQELDLSGTLNVLPEALL 300

QY 301 HLPALOSVSGDVRRCRLVREGTYPRRGSSPKVPLACVDTRESAARGPTIL 353  
Db 301 HLPALOSVSGDVRRCRLVREGTYPRRGSSPKVPLACVDTRESAARGPTIL 353

RESULT 10  
ADD70435 standard; protein; 353 AA.  
XX  
AC ADD70435;  
XX  
DT 15-JAN-2004 (first entry)  
XX  
DE Human secreted/transmembrane protein PRO1788.  
XX  
KW Human; secreted protein; transmembrane protein; PRO; tumour;  
KW immune response; cardiac insufficiency disorder; calcium flux;  
KW umbilical vein endothelial cell; bone disorder; cartilage disorder;  
KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;  
KW Berger disease; neuropathy; Schonlein-Henoch purpura; coeliac disease;  
KW dermatitis; herpeticiformis; Crohn's disease; thalassaemia.  
XX  
OS Homo sapiens.  
XX  
PN US2003054406-A1.  
XX  
PD 20-MAR-2003.  
XX  
PF 06-DEC-2001; 2001US-00006818.  
XX  
PR 01-SEP-1998; 98US-0098716P.  
PR 01-SEP-1998; 98US-0098723P.  
PR 01-SEP-1998; 98US-0098749P.  
PR 01-SEP-1998; 98US-0098750P.  
PR 02-SEP-1998; 98US-0098803P.  
PR 02-SEP-1998; 98US-0098821P.  
PR 02-SEP-1998; 98US-0098843P.  
PR 02-SEP-1998; 98US-0098953P.  
PR 02-SEP-1998; 98US-0099362P.  
PR 02-SEP-1998; 98US-0099388P.  
PR 02-SEP-1998; 98US-0099588P.  
PR 02-SEP-1998; 98US-0099602P.  
PR 02-SEP-1998; 98US-0099642P.  
PR 10-SEP-1998; 98US-0099741P.  
PR 10-SEP-1998; 98US-0099753P.  
PR 10-SEP-1998; 98US-0099782P.  
PR 10-SEP-1998; 98US-0099808P.  
PR 10-SEP-1998; 98US-0099812P.  
PR 10-SEP-1998; 98US-0099815P.  
PR 10-SEP-1998; 98US-0099816P.  
PR 15-SEP-1998; 98US-0100385P.

PR 15-SEP-1998; 98US-0100388P.  
PR 15-SEP-1998; 98US-0100390P.  
PR 16-SEP-1998; 98US-0100384P.  
PR 16-SEP-1998; 98US-0100627P.  
PR 16-SEP-1998; 98US-0100661P.  
PR 16-SEP-1998; 98US-0100662P.  
PR 16-SEP-1998; 98US-0100664P.  
PR 17-SEP-1998; 98US-0100683P.  
PR 17-SEP-1998; 98US-0100684P.  
PR 17-SEP-1998; 98US-0100711P.  
PR 17-SEP-1998; 98US-0100712P.  
PR 17-SEP-1998; 98US-0100930P.  
PR 17-SEP-1998; 98US-0100931P.  
PR 18-SEP-1998; 98US-0100848P.  
PR 18-SEP-1998; 98US-0100849P.  
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PR 18-SEP-1998; 98US-0101068P.  
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 PR 18-NOV-1998; 98US-0108858P.  
 PR 18-NOV-1998; 98US-0108904P.  
 PR 22-DEC-1998; 98US-0113286P.  
 PR 30-DEC-1998; 98US-0114223P.  
 PR 05-JAN-1999; 99WO-US000106.  
 PR 16-APR-1999; 99US-0129674P.  
 PR 23-JUN-1999; 99US-0141037P.  
 PR 20-JUL-1999; 99US-0144758P.  
 PR 26-JUL-1999; 99US-0145698P.  
 PR 01-SEP-1999; 99WO-US020111.  
 PR 15-SEP-1999; 99WO-US021194.  
 PR 29-OCT-1999; 99US-0162506P.  
 PR 30-NOV-1999; 99WO-US028313.  
 PR 02-DEC-1999; 99WO-US028551.  
 PR 16-DEC-1999; 99WO-US030095.  
 PR 05-JAN-2000; 2000WO-US000219.  
 PR 06-JAN-2000; 2000WO-US000376.  
 PR 11-FEB-2000; 2000WO-US003565.  
 PR 18-FEB-2000; 2000WO-US004342.  
 PR 24-FEB-2000; 2000WO-US005004.  
 PR 02-MAR-2000; 2000WO-US005841.  
 PR 15-MAR-2000; 2000WO-US006884.  
 PR 17-MAY-2000; 2000WO-US013705.  
 PR 22-MAY-2000; 2000WO-US014042.  
 PR 30-MAY-2000; 2000WO-US014941.  
 PR 02-JUN-2000; 2000WO-US015264.  
 PR 23-AUG-2000; 2000WO-US023522.  
 PR 24-AUG-2000; 2000WO-US023328.  
 PR 08-NOV-2000; 2000WO-US030952.  
 PR 10-NOV-2000; 2000WO-US030873.  
 PR 01-DEC-2000; 2000WO-US032678.  
 PR 28-FEB-2001; 2001WO-US006520.  
 PR 01-MAR-2001; 2001WO-US006666.  
 PR 01-JUN-2001; 2001WO-US017800.  
 PR 20-JUN-2001; 2001WO-US019692.  
 PR 29-JUN-2001; 2001WO-US021066.  
 PR 09-JUL-2001; 2001WO-US021735.  
 PR 04-SEP-2001; 2001US-00946374.

XX (GETH ) GENENTECH INC.

PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S,  
 PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ,  
 PI Pan J, Paout NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK,  
 PI Williams PM, Wood WI,  
 XX

DR WPI; 2003-708344/67.  
 DR N-PSDB; ADD70434.  
 XX  
 PT Novel isolated PRO polypeptide useful for tissue typing, modulating  
 PT biological activity of cell, as molecular weight markers in protein  
 PT electrophoresis, for treating arthritis, tumor.  
 XX  
 PS Claim 12; SEQ ID NO 397, 549pp; English.  
 XX  
 CC The invention relates to an isolated PRO polypeptide (secreted or

Query Match 100.0%; Score 1828; DB 7; Length 353;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-167;  
 Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPPLLLLAAGCAQTRPCFPCCCEVEETGLFDSFSLTRVDSGLGPHIMPVPIPDT 60  
 DB 1 MNPPLLLLAAGCAQTRPCFPCCCEVEETGLFDSFSLTRVDSGLGPHIMPVPIPDT 60  
 QY 61 AHDLSNRLEWNEVSLAGPEYTTLAGLDLSHNLITISPTAFSRRLVLSLDSHNG 120  
 DB 61 AHDLSNRLEWNEVSLAGPEYTTLAGLDLSHNLITISPTAFSRRLVLSLDSHNG 120  
 QY 121 TALPABFTSSPLSDVNLSHNQLREVSAFTTHSQGALHVDLSHNLHRLVPHPTAG 180  
 DB 121 TALPABFTSSPLSDVNLSHNQLREVSAFTTHSQGALHVDLSHNLHRLVPHPTAG 180  
 QY 181 LPAPTQSLNLAHNLHVAHVNLRDLPLRYLSIDGNPLAVIGGAPAGLGGTLHSLAQ 240  
 DB 181 LPAPTQSLNLAHNLHVAHVNLRDLPLRYLSIDGNPLAVIGGAPAGLGGTLHSLAQ 240  
 QY 241 RLPPLAPSGFRLPGLQVTLDSGNPKLWAGAEVSSGLSIOELDLSGTLVPLPEALL 300  
 DB 241 RLPPLAPSGFRLPGLQVTLDSGNPKLWAGAEVSSGLSIOELDLSGTLVPLPEALL 300  
 QY 301 HLPALQSVGVGDVRCRLVREGTYPRRPGSSPKYPLHCVDTRESAAGPTLL 353  
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RESULT 11  
 ADD38556  
 ID ADD38556 standard; protein; 353 AA.

AC ADD38556;

DT 15-JAN-2004 (first entry)

DE Human secreted/transmembrane protein PRO1788.

XX Human; secreted protein; transmembrane protein; PRO; tumour;  
 KW immune response; cardiac insufficiency disorder; calcium flux;  
 KW umbilical vein endothelial cell; bone disorder; cartilage disorder;  
 KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;  
 KW Berger disease; nephropathy; Schonlein-Henoch purpura; celliac disease;  
 XX dermatitis; herpeticiformis; Crohn's disease; thalassemia.

OS Homo sapiens.

PN US2003096955-A1.

PD 22-MAY-2003.

XX 07-DEC-2001; 2001US-00012755.

PR 01-SEP-1998; 98US-0098716P.  
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 PR 02-SEP-1998; 98US-0098803P.  
 PR 02-SEP-1998; 98US-0098821P.  
 PR 02-SEP-1998; 98US-0098843P.  
 PR 09-SEP-1998; 98US-0099536P.

PR 09-SEP-1998; 98US-009596P.  
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PR 30-DEC-1998; 98US-0114223P.  
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PR 28-FEB-2001; 2001MO-US006520.  
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PR 01-JUN-2001; 2001MO-US017800.

PR 20-JUN-2001; 2001WO-US019692.  
PR 29-JUN-2001; 2001WO-US021066.  
PR 09-JUL-2001; 2001WO-US021735.  
PR 04-SEP-2001; 2001US-00946374.  
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PA (GETH ) GENENTECH INC.  
XX  
PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S,  
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ,  
PI Pan Y, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK,  
PI Williams PM, Wood MI;  
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DR WPI; 2003-787000/74.  
DR N-PSDB; ADD38555.  
XX  
PT Novel isolated PRO polypeptide, useful for treating cancerous tumors,  
PT cardiac insufficiency disorders, wound healing, diabetes mellitus,  
PT thalassemias.  
XX  
PS Claim 12; SEQ ID NO 397; 556bp; English.  
XX  
CC The invention relates to an isolated PRO polypeptide (secreted or  
CC transmembrane protein) having at least 80% amino acid sequence identity  
Query Match 100.0%; Score 1828; DB 7; Length 353;  
Best Local Similarity 100.0%; Pident. No. 1.5e-167; Mismatches 0; Gaps 0;  
Matches 353; Conservative 0; Indels 0;  
QY 1 MPFLLILLAVSAGACTRCPGCGCEVETFGLPDSFSLRVDCSGIGPHIMVPIPLDT 60  
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QY 61 AHDLSNRLDMNVESTIAGPGYTTAGLDLSHNLISIP7AFSRIRYIESLDLSHNL 120  
Db 61 AHDLSNRLDMNVESTIAGPGYTTAGLDLSHNLISIP7AFSRIRYIESLDLSHNL 120  
QY 121 TALPAEFTSSPFLSDVNLSHQREVSVAFTTHSQGRALHVDLSHNLIRLVHPFRAG 180  
Db 121 TALPAEFTSSPFLSDVNLSHQREVSVAFTTHSQGRALHVDLSHNLIRLVHPFRAG 180  
QY 121 TALPAEFTSSPFLSDVNLSHQREVSVAFTTHSQGRALHVDLSHNLIRLVHPFRAG 180  
Db 121 TALPAEFTSSPFLSDVNLSHQREVSVAFTTHSQGRALHVDLSHNLIRLVHPFRAG 180  
QY 181 LPAPTIOSLNLAWRHLAVPNLRDLPRIYSLDGNPLAVIQGAFAGLQVHLISLASLQ 240  
Db 181 LPAPTIOSLNLAWRHLAVPNLRDLPRIYSLDGNPLAVIQGAFAGLQVHLISLASLQ 240  
QY 241 RLPELAFSGFRELPGLOVLDLGNPKLWGAEVFSGLSIQEHLDSGTLNVPRLAL 300  
Db 241 RLPELAFSGFRELPGLOVLDLGNPKLWGAEVFSGLSIQEHLDSGTLNVPRLAL 300  
QY 301 HLPALQSVSVGQDVRCRLVREGTYPRRFGSSPVPLHCVDTRESAARGPTIL 353  
Db 301 HLPALQSVSVGQDVRCRLVREGTYPRRFGSSPVPLHCVDTRESAARGPTIL 353  
RESULT 12  
ADD39512  
ID ADD39512 standard; protein; 353 AA.  
XX  
AC ADD39512;  
XX  
DT 15-JAN-2004 (first entry)  
XX  
DE Human secreted/transmembrane protein PRO1788.  
XX  
KW Human; secreted protein; transmembrane protein; PRO; tumor;  
KW immune response; cardiac insufficiency disorder; calcium flux;  
KW umbilical vein endothelial cell; bone disorder; cartilage disorder;  
KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;  
KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;  
KW dermatitis; herpeticiformis; Crohn's disease; thalassemia.  
XX  
OS Homo sapiens.  
XX  
FN US2003096954-A1.

XX 22-MAY-2003.  
PD 07-DEC-2001; 2001US-00011671.  
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PF  
XX 01-SEP-1998; 98US-0098715P.  
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PR 29-SEP-1998; 98US-0102307P.  
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PR 29-SEP-1998; 98US-0102331P.  
PR 30-SEP-1998; 98US-0102484P.  
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PR 01-OCT-1998; 98US-0102684P.  
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02-MAR-2000; 2000MO-US005841.
PR 15-MAR-2000; 2000MO-US006884.
PR 17-MAY-2000; 2000MO-US013705.
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PR 08-NOV-2000; 2000MO-US030952.
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PR 01-DEC-2000; 2000MO-US032678.
PR 28-FEB-2001; 2001MO-US006520.
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PR 01-JUN-2001; 2001MO-US017800.
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PR 29-JUN-2001; 2001MO-US021066.
PR 09-JUL-2001; 2001MO-US021735.
PR 04-SEP-2001; 2001US-00946374.
XX XX
PA (GETH ) GENENTECH INC.
XX XX
PI Baker KP, Botstein D, Desnoyers L, Baton DL, Ferrara N, Fong S;
PI Gao W, Goddard A, Godowski PJ, Gimaldi JC, Gurney AL, Hillan KJ;
PI Pan Y, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Wetanabe CK;
PI Williams PM, Wood WI;
XX XX
DR MPI; 2003-786999/74.
DR N-PDB; ADD39511.
XX XX
PT Novel isolated PRO polypeptide useful for tissue typing, modulating
PT biological activity of cell, as molecular weight markers in protein
PT electrophoresis, for treating arthritis, tumor.
PS Claim 12; SEQ ID NO 397; 550pp; English.
XX XX
CC The invention relates to an isolated PRO polypeptide (secreted or

Query Match          100.0%; Score 1828; DB 7; Length 353;
Best Local Similarity 100.0%; Pred. No. 1.5e-167; Indels 0; Gaps 0;
Matches 353; Conservative 0; Mismatches 0;

QY      1 MWPLLLILIAVSAGQTRPCPGCGCEVEYFGLPDFSESLRVEDSGLGPHIMVPPIPDT    60
Db      1 MPWPLLIIAIVSAGQTRPCPGCGCEVEYETGTGLDSFLRVDSCGLGPHIMVPPIPDT    60
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QY     121 TALPAESTSTSPILDVNLSHNQLREVSASATFTSSOGRALHYDLSHNLIRLVHPHTTAG   180
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ID      ADD39035 standard; protein; 353 AA.
XX AC
XX ADD39035;
DT      15-JAN-2004 (first entry)

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 PR 04-SEP-2001; 2001US-00946374.  
 XX (GENTH) GENENTECH INC.  
 PA Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S,  
 PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ,  
 PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK,  
 PI Williams PM, Wood WT;  
 XX WPI; 2003-765477/72.  
 DR N-PSDB; ADD39034.  
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XX New isolated PRO polypeptide such as PRO1560, PRO444, PRO1018, PRO1773,  
 PT PRO1244, useful for treating cancerous tumors, cardiac  
 PT insufficiency disorders, wound healing, Crohn's disease, celiac disease.  
 XX Claim 12; SEQ ID NO 397; 555bp; English.  
 PS The invention relates to an isolated PRO polypeptide (secreted or  
 CC

Query March 100.0%; Score 1828; DB 7; Length 353;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-167;  
 Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPWELLILLLVSGAQTTRPCFPQCQCEVETFGGLPDSFSLTRVDCSLGPHIMVPIPLDT 60  
 DB 1 MPWELLILLLVSGAQTTRPCFPQCQCEVETFGGLPDSFSLTRVDCSLGPHIMVPIPLDT 60  
 QY 61 AHLDLSNRLNEMNESVTLAAGTTLAAGLDSHNLTSPTAFSSRLRYESLDSHNGI 120  
 DB 61 AHLDLSNRLNEMNESVTLAAGTTLAAGLDSHNLTSPTAFSSRLRYESLDSHNGI 120  
 QY 121 TALPABSFSTPSLDVNLISHNOLREVSVAFTTHSQGRALHVDLSHNLIRLVPHPTKAG 180  
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 QY 241 RLPETLASSGRELPGLQVLDISGNPKLNMAAEVFSGLSLSQSLDLSGTLVLPFALLL 300  
 DB 241 RLPETLASSGRELPGLQVLDISGNPKLNMAAEVFSGLSLSQSLDLSGTLVLPFALLL 300

QY 301 HLPALQSVSVGQDYRCRRLVREGTYPRRPGSSSPKVLHCVDTRESAARGFTIL 353  
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RESULT 14  
 ID ADD40466  
 AC ADD40466 standard; protein; 353 AA.

XX ADD40466;

DT 15-JAN-2004 (first entry)

DE Human secreted/transmembrane protein PRO1788.

XX Human; secreted protein; transmembrane protein; PRO; tumour;  
 KW immune response; cardiac insufficiency disorder; calcium flux;  
 KW umbilical vein endothelial cell; bone disorder; cartilage disorder;  
 KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;  
 KW Berger disease; neuropathy; Schönlein-Henoch purpura; celiac disease;  
 KW dermatitis; herpeticiformis; Crohn's disease; thalassemia.

XX Homo sapiens.

PN US2003082627-A1.

FD 01-MAY-2003.

PF 06-DEC-2001; 2001US-00006117.

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PR 17-MAY-2000; 2000US-US013705.  
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PR 23-AUG-2000; 2000US-US023522.  
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PR 08-NOV-2000; 2000US-US030952.  
PR 10-NOV-2000; 2000US-US030873.  
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PR 01-JUN-2001; 2001US-US017800.  
PR 20-JUN-2001; 2001US-US019692.  
PR 29-JUN-2001; 2001US-US021066.  
PR 09-JUL-2001; 2001US-US021735.  
PR 04-SEP-2001; 2001US-00946374.  
  
XX (GETH ) GENENTECH INC.  
XX Baker KP, Borstein D, Desnovers L, Eaton DL, Ferrara N, Fong S;  
PI Cao W, Goddard A, Godowski PJ, Grimaldi JC, Guiney AL, Hillan KJ,  
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tamas D, Watanabe CK,  
PI Williams PM, Wood WI;  
XX  
DR MPI; 2003-755104/71.  
XX N-PSDB; ADD40465.  
XX  
PT New isolated PRO polypeptides such as PRO1560, PRO444, PRO1018, PRO1773,  
PT PRO1244, PRO1246, are useful for treating cancerous tumors and cardiac  
PT insufficiency disorders.  
XX  
XX  
XX Claim 12; SEQ ID NO 397; 550bp; English.  
XX  
CC The invention relates to an isolated PRO polypeptide (secreted or  
Query Match 100.0%; Score 1828; DB 7; Length 353;  
Best Local Similarity 100.0%; Pred. No. 1.5e-167;  
Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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RESULT 15  
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XX ADE50687;  
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XX 29-JAN-2004 (first entry)  
DT 29-JAN-2004 (first entry)  
XX  
DE Human secreted/transmembrane protein PRO1788.  
XX  
XX Human; secreted protein; transmembrane protein; PRO; tumour;  
XX immune response; cardiac insufficiency disorder; calcium flux;  
XX umbilical vein endothelial cell; bone disorder; cartilage disorder;  
XX arthritis; wound healing; diabetes; skeletal muscle cells; obesity;  
XX Berger disease; neuropathy; Schonlein-Henoch purpura; colliac disease;  
XX dermatitis; herpeticiformis; Crohn's disease; thalassaemia.  
XX  
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 PR 09-JUL-2001; 2001US-05021735.  
 PR 04-SEP-2001; 2001US-00946374.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S,  
 PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ,  
 PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK,  
 PI Williams PM, Wood WI;  
 XX  
 DR WPI: 2003-708395/67.  
 DR N-PSDB; ADE50686.  
 PT Novel secreted and transmembrane PRO polypeptides useful in the  
 PT preparation of a medicament for treating a condition responsive to PRO  
 PT polypeptide and as therapeutic agents e.g. vaccines.  
 XX  
 PS Claim 12; SEQ ID NO 397; 555pp; English.

XX  
 CC The invention relates to an isolated PRO polypeptide (secreted or  
 Query Match 100.0%; Score 1828; DB 7; Length 353;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-167;  
 Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MEMPLILLAVSGAQTTRPCFPGCCCEVEFTGLFDSFSLTRVDCSGLPHMPVPIPIDT 60  
 DB 1 MEMPLILLAVSGAQTTRPCFPGCCCEVEFTGLFDSFSLTRVDCSGLPHMPVPIPIDT 60  
 QY 61 AHLDSSNRLEWNEVSVLAGEYTTLAGLDLSHNLITISPTAFRLRYLSLDSHNGL 120  
 DB 61 AHLDSSNRLEWNEVSVLAGEYTTLAGLDLSHNLITISPTAFRLRYLSLDSHNGL 120  
 QY 121 TALPAESFTSSPLSDVNLISHNQLREVSVSAFTTHSQGALHVDLSHNLIRLVPHPTAG 180  
 DB 121 TALPAESFTSSPLSDVNLISHNQLREVSVSAFTTHSQGALHVDLSHNLIRLVPHPTAG 180  
 QY 181 LPAPTIGSINLAWNLHAAVPIRLDPLRYLSLDGNPLAVIGPAGAGLGLTHSLASLQ 240  
 DB 181 LPAPTIGSINLAWNLHAAVPIRLDPLRYLSLDGNPLAVIGPAGAGLGLTHSLASLQ 240  
 QY 241 RLEPLAPSGFRELPGLOVLDLSGNPKLWAGAEVSSLSQELDLSGTNLVLPPEALL 300  
 DB 241 RLEPLAPSGFRELPGLOVLDLSGNPKLWAGAEVSSLSQELDLSGTNLVLPPEALL 300  
 QY 301 HLPALQSVSGQDVRCRLVREGTYPRRGSSPKVPLCHCVTRBSAARGPTIL 353  
 DB 301 HLPALQSVSGQDVRCRLVREGTYPRRGSSPKVPLCHCVTRBSAARGPTIL 353  
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 Job time : 67 secs





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102	144.5	7.9	348	1	US-08-366-953A-45	Sequence 45, Appl	175	711	6.6	711	4	US-09-228-986-79	Sequence 79, Appl
103	144.5	7.9	348	2	US-08-484-397A-2	Sequence 2, Appl	176	121	6.6	4339	4	US-09-052-469-6	Sequence 6, Appl
104	144.5	7.9	348	2	US-08-484-397A-3	Sequence 3, Appl	177	121	6.6	4339	4	US-08-422-582-6	Sequence 6, Appl
105	144.5	7.9	348	2	US-08-484-397A-4	Sequence 4, Appl	178	121	6.6	4339	4	US-09-052-262-6	Sequence 6, Appl
106	144.5	7.9	348	2	US-08-484-397A-5	Sequence 5, Appl	179	120	6.6	305	4	US-09-325-932A-188	Sequence 188, App
107	144.5	7.9	348	2	US-08-484-397A-6	Sequence 6, Appl	180	16.5	6.4	180	3	US-08-986-485-8	Sequence 8, Appl
108	144.5	7.9	348	2	US-08-484-397A-7	Sequence 7, Appl	181	16.5	6.4	268	3	US-09-353-885-6	Sequence 6, Appl
109	144.5	7.9	348	2	US-08-484-397A-27	Sequence 27, Appl	182	116.5	6.4	327	4	US-09-513-505-14	Sequence 14, Appl
110	144.5	7.9	348	2	US-08-484-397A-38	Sequence 38, Appl	183	114.5	6.3	1248	4	US-10-042-810-2	Sequence 2, Appl
111	144.5	7.9	348	2	US-08-484-397A-2	Sequence 2, Appl	184	114.5	6.3	1278	4	US-10-042-810-4	Sequence 4, Appl
112	144.5	7.9	348	2	US-08-484-397A-2	Sequence 2, Appl	185	114	6.2	327	1	US-08-238-163-4	Sequence 4, Appl
113	144.5	7.9	348	2	US-08-484-397A-2	Sequence 2, Appl	186	114	6.2	366	3	US-08-746-883-6	Sequence 6, Appl
114	144.5	7.9	348	2	US-08-484-397A-2	Sequence 2, Appl	187	114	6.2	366	3	US-09-313-177-6	Sequence 6, Appl
115	144.5	7.9	348	2	US-08-484-397A-2	Sequence 2, Appl	188	114	6.2	427	3	US-08-448-122A-4	Sequence 4, Appl
116	144.5	7.9	348	2	US-08-484-397A-2	Sequence 2, Appl	189	114	6.2	427	3	US-08-189-1098A-4	Sequence 4, Appl
117	144.5	7.9	348	2	US-08-484-397A-2	Sequence 2, Appl	190	114	6.2	134	3	US-09-161-647-12	Sequence 12, Appl
118	144.5	7.9	348	2	US-08-484-397A-2	Sequence 2, Appl	191	113.5	6.2	134	3	US-09-540-245A-12	Sequence 12, Appl
119	144.5	7.9	348	2	US-08-484-397A-2	Sequence 2, Appl	192	113.5	6.2	134	3	US-09-540-245A-12	Sequence 12, Appl
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121	144.5	7.9	348	2	US-08-484-397A-2	Sequence 2, Appl	194	113	6.2	692	4	US-08-461-657B-6	Sequence 6, Appl
122	144.5	7.9	348	2	US-08-484-397A-2	Sequence 2, Appl	195	113	6.2	1240	4	US-08-930-996A-4	Sequence 4, Appl
123	144.5	7.9	348	2	US-08-484-397A-2	Sequence 2, Appl	196	111.5	6.1	301	3	US-09-353-585-5	Sequence 5, Appl
124	144.5	7.9	348	2	US-08-484-397A-2	Sequence 2, Appl	197	111.5	6.1	359	4	US-09-842-164A-4	Sequence 4, Appl
125	144.5	7.9	348	2	US-08-484-397A-2	Sequence 2, Appl	198	111.5	6.1	825	1	US-07-912-952-2	Sequence 2, Appl
126	144.5	7.9	348	2	US-08-484-397A-2	Sequence 2, Appl	199	111	6.1	825	1	US-08-359-705B-8	Sequence 8, Appl
127	144.5	7.9	348	2	US-08-484-397A-2	Sequence 2, Appl	200	111	6.1	612	2	US-08-286-846A-8	Sequence 8, Appl
128	144.5	7.9	348	2	US-08-484-397A-2	Sequence 2, Appl	201	111	6.1	612	2	US-08-457-880A-8	Sequence 8, Appl
129	144.5	7.9	348	2	US-08-484-397A-2	Sequence 2, Appl	202	111	6.1	612	2	US-08-444-622A-8	Sequence 8, Appl
130	144.5	7.9	348	2	US-08-484-397A-2	Sequence 2, Appl	203	111	6.1	612	2	US-08-942-562-8	Sequence 8, Appl
131	144.5	7.9	348	2	US-08-484-397A-2	Sequence 2, Appl	204	111	6.1	612	2	US-09-156-923-8	Sequence 8, Appl
132	144.5	7.9	348	2	US-08-484-397A-2	Sequence 2, Appl	205	111	6.1	612	2	US-08-359-705B-8	Sequence 8, Appl
133	144.5	7.9	348	2	US-08-484-397A-2	Sequence 2, Appl	206	111	6.1	839	2	US-08-286-846A-6	Sequence 6, Appl
134	144.5	7.9	348	2	US-08-484-397A-2	Sequence 2, Appl	207	111	6.1	839	2	US-08-457-880A-6	Sequence 6, Appl
135	144.5	7.9	348	2	US-08-484-397A-2	Sequence 2, Appl	208	111	6.1	839	2	US-08-444-622A-6	Sequence 6, Appl
136	144.5	7.9	348	2	US-08-484-397A-2	Sequence 2, Appl	209	111	6.1	839	2	US-08-942-562-8	Sequence 8, Appl
137	144.5	7.9	348	2	US-08-484-397A-2	Sequence 2, Appl	210	111	6.1	839	2	US-08-457-880A-6	Sequence 6, Appl
138	144.5	7.9	348	2	US-08-484-397A-2	Sequence 2, Appl	211	110.5	6.0	850	2	US-08-444-622A-6	Sequence 6, Appl
139	144.5	7.9	348	2	US-08-484-397A-2	Sequence 2, Appl	212	110.5	6.0	850	2	US-08-444-622A-6	Sequence 6, Appl
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144	144.5	7.9	348	2	US-08-484-397A-2	Sequence 2, Appl	217	109	6.0	764	3	US-07-741-453A-60	Sequence 60, Appl
145	144.5	7.9	348	2	US-08-484-397A-2	Sequence 2, Appl	218	109	6.0	764	3	US-07-741-453A-60	Sequence 60, Appl
146	144.5	7.9	348	2	US-08-484-397A-2	Sequence 2, Appl	219	109	6.0	764	3	US-07-741-453A-60	Sequence 60, Appl
147	144.5	7.9	348	2	US-08-484-397A-2	Sequence 2, Appl	220	109	6.0	764	3	US-07-741-453A-60	Sequence 60, Appl
148	144.5	7.9	348	2	US-08-484-397A-2	Sequence 2, Appl	221	109	6.0	764	3	US-07-741-453A-60	Sequence 60, Appl
149	144.5	7.9	348	2	US-08-484-397A-2	Sequence 2, Appl	222	109	6.0	764	3	US-07-741-453A-60	Sequence 60, Appl
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152	144.5	7.9	348	2	US-08-484-397A-2	Sequence 2, Appl	225	109	6.0	764	3	US-07-741-453A-60	Sequence 60, Appl
153	144.5	7.9	348	2	US-08-484-397A-2	Sequence 2, Appl	226	109	6.0	764	3	US-07-741-453A-60	Sequence 60, Appl
154	144.5	7.9	348	2	US-08-484-397A-2	Sequence 2, Appl	227	109	6.0	764	3	US-07-741-453A-60	Sequence 60, Appl
155	144.5	7.9	348	2	US-08-484-397A-2	Sequence 2, Appl	228	109	6.0	764	3	US-07-741-453A-60	Sequence 60, Appl
156	144.5	7.9	348	2	US-08-484-397A-2	Sequence 2, Appl	229	109	6.0	764	3	US-07-741-453A-60	Sequence 60, Appl
157	144.5	7.9	348	2	US-08-484-397A-2	Sequence 2, Appl	230	109	6.0	764	3	US-07-741-453A-60	Sequence 60, Appl
158	144.5	7.9	348	2	US-08-484-397A-2	Sequence 2, Appl	231	109	6.0	764	3	US-07-741-453A-60	Sequence 60, Appl
159	144.5	7.9	348	2	US-08-484-397A-2	Sequence 2, Appl	232	109	6.0	764	3	US-07-741-453A-60	Sequence 60, Appl
160	144.5	7.9	348	2	US-08-484-397A-2	Sequence 2, Appl	233	109	6.0	764	3	US-07-741-453A-60	Sequence 60, Appl
161	144.5	7.9	348	2	US-08-484-397A-2	Sequence 2, Appl	234	109	6.0	764	3	US-07-741-453A-60	Sequence 60, Appl
162	144.5	7.9	348	2	US-08-484-397A-2	Sequence 2, Appl	235	109	6.0	764	3	US-07-741-453A-60	Sequence 60, Appl
163	144.5	7.9	348	2	US-08-484-397A-2	Sequence 2, Appl	236	109	6.0	764	3	US-07-741-453A-60	Sequence 60, Appl
164	144.5	7.9	348	2	US-08-484-397A-2	Sequence 2, Appl	237	109	6.0	764	3	US-07-741-453A-60	Sequence 60, Appl
165	144.5	7.9	348	2	US-08-484-397A-2	Sequence 2, Appl	238	109	6.0	764	3	US-07-741-453A-60	Sequence 60, Appl
166	144.5	7.9	348	2	US-08-484-397A-2	Sequence 2, Appl	239	109	6.0	764	3	US-07-741-453A-60	Sequence 60, Appl
167	144.5	7.9	348	2	US-08-484-397A-2	Sequence 2, Appl	240	109	6.0	764	3	US-07-741-453A-60	Sequence 60, Appl
168	144.5	7.9	348	2	US-08-484-397A-2	Sequence 2, Appl	241	109	6.0	764	3	US-07-741-453A-60	Sequence 60, Appl
169	144.5	7.9	348	2	US-08-484-397A-2	Sequence 2, Appl	242	109	6.0	764	3	US-07-741-453A-60	Sequence 60, Appl
170	144.5	7.9	348	2	US-08-484-397A-2	Sequence 2, Appl	243	109	6.0	764	3	US-07-741-453A-60	Sequence 60, Appl
171	144.5	7.9	348	2	US-08-484-397A-2	Sequence 2, Appl	244	109	6.0	764	3	US-07-741-453A-60	Sequence 60, Appl
172	144.5	7.9	348	2	US-08-484-397A-2	Sequence 2, Appl	245	109	6.0	764	3	US-07-741-453A-60	Sequence 60, Appl
173	144.5	7.9	348	2	US-08-484-397A-2	Sequence 2, Appl	246	109	6.0	764	3	US-07-741-453A-60	Sequence 60, Appl



247	99.5	5.4	1005	4	US-09-134-0306-6332	Sequence 6322, App	320	92	5.0	677	3	US-08-836-567-2	Sequence 2, App1
248	99	5.4	1435	2	US-08-531-439B-108	Sequence 108, App1	321	92	5.0	677	3	US-09-606-304-2	Sequence 2, App1
249	99	5.4	1143	2	US-08-310-512A-108	Sequence 108, App	322	92	5.0	1197	3	US-08-836-567-12	Sequence 12, App1
250	99	5.4	1143	5	US-09-301-085-108	Sequence 108, App	323	92	5.0	1197	3	US-08-836-567-12	Sequence 12, App1
251	99	5.4	1143	5	PCT-US95-04589-108	Sequence 2, App1	324	92	5.0	1230	2	US-08-968-342C-5	Sequence 35, App1
252	99	5.4	1144	1	US-08-261-663A-2	Sequence 4, App1	325	91.5	5.0	1230	2	US-09-555-467A-15	Sequence 35, App1
253	99	5.4	1144	1	US-08-261-663A-4	Sequence 4, App1	326	91.5	5.0	415	4	US-09-252-991A-22392	Sequence 22392, App1
254	99	5.4	1144	4	US-09-357-206A-3	Sequence 3, App1	327	91.5	5.0	544	4	US-09-396-154-14	Sequence 14, App1
255	99	5.4	1144	4	US-09-357-206A-3	Sequence 2, App1	328	91.5	5.0	544	4	US-09-396-154-14	Sequence 20, App1
256	99	5.4	1144	4	PCT-US95-07754A-2	Sequence 4, App1	329	91.5	5.0	655	4	US-09-328-986-70	Sequence 70, App1
257	99	5.4	1144	4	PCT-US95-07754A-4	Sequence 6359, App	330	91.5	5.0	1220	3	US-08-930-986A-2	Sequence 2, App1
258	98.5	5.4	732	4	US-09-134-000C-6359	Sequence 8, App1	331	91	5.0	419	4	US-09-630-155-2	Sequence 2, App1
259	98	5.4	155	3	US-09-191-647-8	Sequence 8, App1	332	91	5.0	690	4	US-09-543-681A-6677	Sequence 4677, App
260	98	5.4	155	3	US-09-540-245A-8	Sequence 8, App1	333	91	5.0	740	4	US-10-164-595-6	Sequence 6, App1
261	98	5.4	155	3	US-09-540-153-8	Sequence 8, App1	334	91	5.0	755	4	US-10-164-595-10	Sequence 10, App1
262	98	5.4	155	3	US-09-540-153-3	Sequence 3, App1	335	90.5	5.0	781	4	US-10-164-595-4	Sequence 4, App1
263	98	5.4	821	1	US-08-489-039A-13033	Sequence 13033, A	336	90.5	5.0	191	4	US-09-461-325-186	Sequence 186, App
264	97.5	5.3	530	4	US-08-339-578-2	Sequence 3, App1	337	90.5	5.0	191	4	US-10-012-542-166	Sequence 186, App
265	97	5.3	105	3	US-08-466-049-3	Sequence 3, App1	338	90.5	5.0	728	1	US-07-912-952-4	Sequence 4, App1
266	97	5.3	105	3	US-09-161-647-3	Sequence 3, App1	339	90	4.9	526	4	US-09-252-991A-28402	Sequence 28402, App1
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287	96	5.3	907	3	US-08-930-996A-7	Sequence 7, App1	360	89	4.9	674	4	US-07-757-342D-10	Sequence 10, App1
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484 82 4.5 988 4 US-09-252-991A-17380 Sequence 17380, A  
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497 81.5 4.5 605 4 US-09-252-991A-18837 Sequence 18837, A  
498 81.5 4.5 920 4 US-09-564-605-28 Sequence 28, App  
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## ALIGNMENTS

RESULT 1  
US-09-907-794A-245  
; Sequence 245, Application US/09907794A  
; Patent No. 6635468  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Askenazi, Avi  
; APPLICANT: Botstein, David  
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; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William, I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: 10466-14

CURRENT APPLICATION NUMBER: US/09/907,794A  
CURRENT FILING DATE: 2001-07-17  
PRIOR APPLICATION NUMBER: PCT/US00/04414  
PRIOR FILING DATE: 2000-02-22  
PRIOR APPLICATION NUMBER: US 60/143,048  
PRIOR FILING DATE: 1999-07-07  
PRIOR APPLICATION NUMBER: US 60/145,698  
PRIOR FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: US 60/146,222  
PRIOR FILING DATE: 1999-07-28  
PRIOR APPLICATION NUMBER: PCT/US99/20594  
PRIOR FILING DATE: 1999-09-08  
PRIOR APPLICATION NUMBER: PCT/US99/20944  
PRIOR FILING DATE: 1999-09-13  
PRIOR APPLICATION NUMBER: PCT/US99/21090  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/21547  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/23089  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: PCT/US99/28214  
PRIOR FILING DATE: 1999-11-29  
PRIOR APPLICATION NUMBER: PCT/US99/28313  
PRIOR FILING DATE: 1999-11-30  
PRIOR APPLICATION NUMBER: PCT/US99/28564  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/28565  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/30095  
PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: PCT/US99/30911  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US99/30999  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US00/00219  
NUMBER OF SEQ ID NOS: 423  
SEQ ID NO 245  
LENGTH: 713  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-09-907-794A-245

Query Match 17.4%; Score 318.5; DB 4; Length 713;  
Best Local Similarity 27.6%; Pred. No. 3.3e-21;  
Matches 115; Conservative 55; Mismatches 161; Indels 85; Gaps 11;

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RESULT 2  
US-09-905-125A-245  
Sequence 245, Application US/09905125A  
Patent No. 6664376  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Filvarolt, Ellen  
APPLICANT: Fong, Sherman  
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APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertlsen, Mary E.  
APPLICANT: Goddard, A.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gueney, Austin L.  
APPLICANT: Hillan, Kenneth, J.  
APPLICANT: Kijavitt, Ivar J.  
APPLICANT: Mather, Jennie P.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William, I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: 10466-14  
CURRENT APPLICATION NUMBER: US/09/905,125A  
CURRENT FILING DATE: 2001-07-12  
PRIOR APPLICATION NUMBER: PCT/US00/04414  
PRIOR FILING DATE: 2000-02-22  
PRIOR APPLICATION NUMBER: US 60/143,048  
PRIOR FILING DATE: 1999-07-07  
PRIOR APPLICATION NUMBER: US 60/145,698  
PRIOR FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: PCT/US99/21090  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/21547  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/20594  
PRIOR FILING DATE: 1999-09-08  
PRIOR APPLICATION NUMBER: PCT/US99/20944  
PRIOR FILING DATE: 1999-09-13  
PRIOR APPLICATION NUMBER: PCT/US99/28214  
PRIOR FILING DATE: 1999-11-29  
PRIOR APPLICATION NUMBER: PCT/US99/28313  
PRIOR FILING DATE: 1999-11-30  
PRIOR APPLICATION NUMBER: PCT/US99/28564  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/28565  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/30095  
PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: PCT/US99/30911  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US99/30999  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US00/00219  
NUMBER OF SEQ ID NOS: 423

SEQ ID NO 245  
 LENGTH: 713  
 TYPE: PRT  
 ORGANISM: Homo Sapien  
 US-09-905-125A-245

Query Match 17.4%; Score 318.5; DB 4; Length 713;  
 Best Local Similarity 27.6%; Pred. No. 3.3e-21;  
 Matches 115; Conservative 55; Mismatches 161; Indels 85; Gaps 11;

QY 6 LLLAVSGAQT-----RCPPGCCCEVETGGLDSF--SLTRVDCSGGLGHIMPVI 56  
 DB 8 LLLAVAGATATVPVPMHVPCCPQCAQIRPMTYRPSSTREATTVDGNDLFTAVPPAL 67  
 QY 57 PLDTAHLDSNRLEWNEVESVLAGPGY-TTLAGLDLSHNLITISPTAFSRRLYESLDL 115  
 DB 68 PAGTQTLLQNSIVRVDSGL--GYLANLTLELDLQNSFSFSDARCDCHALPQLLSLHL 124  
 QY 116 SHNGITLPAESFTS-SPLSDVNLSHNOLREVSVSAFTTHSQGRLHVDLSHNLHRLVP 174  
 DB 125 EENQTLREDSFAGLASLOELYLNHQLYRIAPRAFSGLSNLRLH--LNSNLRAL-- 180  
 QY 175 HPRAGLPARTIOSLNLAMRLHAV-----PNLRDL----- 205  
 DB 181 -DSRFEMLPNLEILMGKXVDALIDMNPRLANLSVLAGNMLREISDYALEGQSL 239  
 QY 206 -----PLRYSLDGNPLAVIGPQAFAGLGLTHLSLASLQRLP 243  
 DB 240 ESLSFYDNLQARVPRALQVPGKFLDNLNKPQGVGPDGFANMLHKLGLNNMELV 299  
 QY 244 ELAPSGRELPGQVLDLSGNPKLNAGAEVFSGLSSLOSLDLSGTNLVPLPEALLHL 303  
 DB 300 SIDKPALVNLBELTLDITNNPRLSFTHPRAFHLPQMETLMMNNALSALHQGVESLP 359  
 QY 304 ALQSVSV-GQDVRCRLVR-----EGTYPRRPGSSPKVPLHCVDTR 344  
 DB 360 NLQEVGLHGNPIRCDVIRMANATGTRVRFIEPOSTLCAEPDQLQRLPVREVPFE 415

RESULT 3  
 US-09-902-775A-245  
 Sequence 245, Application US/09902775A  
 Patent No. 6686451  
 GENERAL INFORMATION:

APPLICANT: Genentech, Inc.  
 APPLICANT: Ashtkenazi, Avi  
 APPLICANT: Botstein, David  
 APPLICANT: Desnoyers, Luc  
 APPLICANT: Eaton, Dan L.  
 APPLICANT: Ferrara, Napoleone  
 APPLICANT: Filvaroff, Ellen  
 APPLICANT: Fong, Sherman  
 APPLICANT: Gao, Wei-Qiang  
 APPLICANT: Gerber, Hanspeter  
 APPLICANT: Gerritsen, Mary E.  
 APPLICANT: Goddard, A.  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Grimaldi, Christopher J.  
 APPLICANT: Gurley, Austin L.  
 APPLICANT: Hillan, Kenneth, J.  
 APPLICANT: Kijavrin, Ivar J.  
 APPLICANT: Macher, Jennie P.  
 APPLICANT: Pan, James  
 APPLICANT: Paoni, Nicholas F.  
 APPLICANT: Roy, Margaret Ann  
 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William, I.  
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 FILE REFERENCE: 10466-14  
 CURRENT APPLICATION NUMBER: US/09/902,775A

CURRENT FILING DATE: 2001-07-10  
 PRIOR APPLICATION NUMBER: PCT/US00/04414  
 PRIOR FILING DATE: 2000-02-22  
 PRIOR APPLICATION NUMBER: US 60/143,048  
 PRIOR FILING DATE: 1999-07-07  
 PRIOR APPLICATION NUMBER: US 60/145,698  
 PRIOR FILING DATE: 1999-07-26  
 PRIOR APPLICATION NUMBER: US 60/146,222  
 PRIOR FILING DATE: 1999-07-28  
 PRIOR APPLICATION NUMBER: PCT/US99/20594  
 PRIOR FILING DATE: 1999-09-08  
 PRIOR APPLICATION NUMBER: PCT/US99/20944  
 PRIOR FILING DATE: 1999-09-13  
 PRIOR APPLICATION NUMBER: PCT/US99/21090  
 PRIOR FILING DATE: 1999-09-15  
 PRIOR APPLICATION NUMBER: PCT/US99/21547  
 PRIOR FILING DATE: 1999-09-15  
 PRIOR APPLICATION NUMBER: PCT/US99/23089  
 PRIOR FILING DATE: 1999-10-05  
 PRIOR APPLICATION NUMBER: PCT/US99/28214  
 PRIOR FILING DATE: 1999-11-29  
 PRIOR APPLICATION NUMBER: PCT/US99/28313  
 PRIOR FILING DATE: 1999-11-30  
 PRIOR APPLICATION NUMBER: PCT/US99/28564  
 PRIOR FILING DATE: 1999-12-02  
 PRIOR APPLICATION NUMBER: PCT/US99/28565  
 PRIOR FILING DATE: 1999-12-02  
 PRIOR APPLICATION NUMBER: PCT/US99/30095  
 PRIOR FILING DATE: 1999-12-16  
 PRIOR APPLICATION NUMBER: PCT/US99/30911  
 PRIOR FILING DATE: 1999-12-20  
 PRIOR APPLICATION NUMBER: PCT/US99/30999  
 PRIOR FILING DATE: 1999-12-20  
 PRIOR APPLICATION NUMBER: PCT/US00/00219  
 PRIOR FILING DATE: 2000-01-05  
 NUMBER OF SEQ ID NOS: 423  
 SEQ ID NO 245  
 LENGTH: 713  
 TYPE: PRT  
 ORGANISM: Homo Sapien  
 US-09-902-775A-245

Query Match 17.4%; Score 318.5; DB 4; Length 713;  
 Best Local Similarity 27.6%; Pred. No. 3.3e-21;  
 Matches 115; Conservative 55; Mismatches 161; Indels 85; Gaps 11;

QY 6 LLLAVSGAQT-----RCPPGCCCEVETGGLDSF--SLTRVDCSGGLGHIMPVI 56  
 DB 8 LLLAVAGATATVPVPMHVPCCPQCAQIRPMTYRPSSTREATTVDGNDLFTAVPPAL 67  
 QY 57 PLDTAHLDSNRLEWNEVESVLAGPGY-TTLAGLDLSHNLITISPTAFSRRLYESLDL 115  
 DB 68 PAGTQTLLQNSIVRVDSGL--GYLANLTLELDLQNSFSFSDARCDCHALPQLLSLHL 124  
 QY 116 SHNGITLPAESFTS-SPLSDVNLSHNOLREVSVSAFTTHSQGRLHVDLSHNLHRLVP 174  
 DB 125 EENQTLREDSFAGLASLOELYLNHQLYRIAPRAFSGLSNLRLH--LNSNLRAL-- 180  
 QY 175 HPRAGLPARTIOSLNLAMRLHAV-----PNLRDL----- 205  
 DB 181 -DSRFEMLPNLEILMGKXVDALIDMNPRLANLSVLAGNMLREISDYALEGQSL 239  
 QY 206 -----PLRYSLDGNPLAVIGPQAFAGLGLTHLSLASLQRLP 243  
 DB 240 ESLSFYDNLQARVPRALQVPGKFLDNLNKPQGVGPDGFANMLHKLGLNNMELV 299  
 QY 244 ELAPSGRELPGQVLDLSGNPKLNAGAEVFSGLSSLOSLDLSGTNLVPLPEALLHL 303  
 DB 300 SIDKPALVNLBELTLDITNNPRLSFTHPRAFHLPQMETLMMNNALSALHQGVESLP 359  
 QY 304 ALQSVSV-GQDVRCRLVR-----EGTYPRRPGSSPKVPLHCVDTR 344  
 DB 360 NLQEVGLHGNPIRCDVIRMANATGTRVRFIEPOSTLCAEPDQLQRLPVREVPFE 415

Query Match	14.5%;	Score 265;	DB 4;	Length 907;
Best Local Similarity	30.1%;	Pred. No. 5.1e-16;		

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Db      86  ---YSTDFPVNLGDLDSQNNLSVTINIVKMPQLLSVLEENKLTPEKCLSELNLT 142
QY      134 SDVNLSHNOJREVSVSAFTTHSGRLHYD-----LSHNLHR 171
Db      143 QELVYNHNLSTISPGAFGLHNLRLHNSNRLQMINSKWPDALPNEILMGENPILR 202
QY      172 L-----VHPPTAGLPAPTIOSLNLMNRHLAVPNL---RDL 205
Db      203 IKMNMKPLINRSVYAGINLIEIDNMLVGL--ENESISFYDNRLIKVPHVALQKV 260
QY      206 PLRYSLDGNPLAVIGPGAFAGLGLTHLSLASLQRLPELAPSGFRELPGLOVLDLSCNP 265
Db      261 NLKFLDLNKNPILNIRRGDFSNMLHKELGINNMPELISDLSLVNDLPDLRKIEATNTP 320
QY      266 KLMWAGAEVSGSLISQELDLSGNTLVPLPEALLHLPALQSVY-GQDVRCRLVR--- 321
Db      321 RLSTYIHNAFFRLPKLESLMNSNLSALYHGTIBSLNKLKISHSNPIRCDVCIRMMN 380
QY      322 -EGTYPR--RPGSSPKVPLHCVDTRE 344
Db      381 MNKTNIRFMEPDS-----LFCVDPE 401

RESULT 9
US-09-905-125A-69
; Sequence 69, Application US/09905125A
; Patent No. 6664376
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurley, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavich, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Paoni, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Thomas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secretd and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,125A
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15

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; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 69
; LENGTH: 708
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-905-125A-69

Query Match      13.9%; Score 254; DB 4; Length 708;
Best Local Similarity 25.1%; Pred. No. 3.8e-15;
Matches 97; Conservative 63; Mismatches 144; Indels 82; Gaps 13;

QY      24 COCEVETGELPDSFSL-----TRVDCSGGPHIMPVPIPLDRAHDLPSNRLEWVESVLA 79
Db      33 CTCEIRPW--FTPRSTYNEASTVDCNDJGLTFPRLPRLANTQIILLQNNIAKIE----- 85
QY      80 GPGYTT-----LAGDLSHNLTSISPTAFSRRLRYLESGLDSHNGTALPAESFTS--SPL 133
Db      86 ---YSTDFPVNLGDLDSQNNLSVTINIVKMPQLLSVLEENKLTPEKCLSELNLT 142
QY      134 SDVNLSHNOJREVSVSAFTTHSGRLHYD-----LSHNLHR 171
Db      143 QELVYNHNLSTISPGAFGLHNLRLHNSNRLQMINSKWPDALPNEILMGENPILR 202
QY      172 L-----VHPPTAGLPAPTIOSLNLMNRHLAVPNL---RDL 205
Db      203 IKMNMKPLINRSVYAGINLIEIDNMLVGL--ENESISFYDNRLIKVPHVALQKV 260
QY      206 PLRYSLDGNPLAVIGPGAFAGLGLTHLSLASLQRLPELAPSGFRELPGLOVLDLSCNP 265
Db      261 NLKFLDLNKNPILNIRRGDFSNMLHKELGINNMPELISDLSLVNDLPDLRKIEATNTP 320
QY      266 KLMWAGAEVSGSLISQELDLSGNTLVPLPEALLHLPALQSVY-GQDVRCRLVR--- 321
Db      321 RLSTYIHNAFFRLPKLESLMNSNLSALYHGTIBSLNKLKISHSNPIRCDVCIRMMN 380
QY      322 -EGTYPR--RPGSSPKVPLHCVDTRE 344
Db      381 MNKTNIRFMEPDS-----LFCVDPE 401

RESULT 10
US-09-902-775A-69
; Sequence 69, Application US/09902775A
; Patent No. 6686451
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman

```



APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltsen, Mary E.  
APPLICANT: Goddard, A.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth, J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Mather, Jennie P.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William, I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: 10466-14  
CURRENT APPLICATION NUMBER: US/09/902, 775A  
CURRENT FILING DATE: 2001-07-10  
PRIOR APPLICATION NUMBER: PCT/US00/04414  
PRIOR FILING DATE: 2000-02-22  
PRIOR APPLICATION NUMBER: US 60/143, 048  
PRIOR FILING DATE: 1999-07-07  
PRIOR APPLICATION NUMBER: US 60/145, 698  
PRIOR FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: US 60/146, 222  
PRIOR FILING DATE: 1999-07-28  
PRIOR APPLICATION NUMBER: PCT/US99/20594  
PRIOR FILING DATE: 1999-09-08  
PRIOR APPLICATION NUMBER: PCT/US99/20944  
PRIOR FILING DATE: 1999-09-13  
PRIOR APPLICATION NUMBER: PCT/US99/21090  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/21547  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/23089  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: PCT/US99/28214  
PRIOR FILING DATE: 1999-11-29  
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PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US99/30999  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US00/00219  
PRIOR FILING DATE: 2000-01-05  
NUMBER OF SEQ ID NOS: 423  
SEQ ID NO 69  
LENGTH: 708  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-902-775A-69

Query Match 13.9%; Score 254; DB 4; Length 708;  
Best Local Similarity 25.1%; Pred. No. 3.8e-15;  
Matches 97; Conservative 63; Mismatches 144; Indels 82; Gaps 13;

QY 24 COCEVETFGIFDSFSL---TRVDCSGIGHIMIPVPIPIDTHAHLDDSSNRLEMNESVLA 79  
DB 33 CTEIRPW--FTRRSYMERASTYDCNDLGLTFPAFLPANTQILLQTNINIKIR----- 85  
QY 80 GPCYTT-----TAGLDLSHLLTSISPTAFSRURKYLESDLSHNGITLPAESFTS--SPL 133

DB 86 ---YSTDFPVNLGLDLSÖNNLSSVTININVKMPÖLISVYLEENKTELPEKLSLSNL 142  
QY 134 SDVNLISHNÖREVSVAFTTHSQRALHVD-----LSHNLIR 171  
DB 143 QELIYNNLLSTISPGAFIGLHMLRLHNSNRLÖMINSKFPALPMLLETIMGENPIIR 202  
QY 172 L-----VPHPTAGPAPPIÖGLNANRLHAVPML---RDL 205  
DB 203 IKDNNFKPLINRLSLVAGINLTFIPNNALVGL--ENLESISFYDRLIVPVALÖKV 260  
QY 206 PLYSLSDGNPLAVIGGAFAGLGLTHLSLASLÖRLPELAPSGFRELPGÖVLDSGN 265  
DB 261 NLKFLDANKPINKPINKRGDFSNNMLHKEGLNNMPELISDLSLVNLPPLRKITEATNP 320  
QY 266 KLNAGAEVSGSLLELDLSTNVLVPEALILHPALÖSVV--GÖDYRCRLYR--- 321  
DB 321 FLSTYHPNAPFRIPKESLMSNLSVALHYGTIESLPNKEISIHSPNRCDCVIRMMN 380  
QY 322 -EGTYPR--RPGSSPKVPLHCVDPR 344  
DB 381 MKNTINRPMEDS-----LFCVDPP 401

RESULT 11  
US-08-592-500-2  
Sequence 2, Application US/08592500  
Patent No. 6005089  
GENERAL INFORMATION:  
APPLICANT: Lanza, Francois  
APPLICANT: Phillips, David R.  
APPLICANT: Cazenave, Jean-Pierre  
TITLE OF INVENTION: Platelet Glycoprotein V Gene and Uses  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSES: Townsend and Townsend Kourie and Crew  
STREET: 379 Lytcon Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patentia Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/592,500  
FILING DATE:  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/089,455  
FILING DATE: 09-JUL-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Dow, Karen B.  
REGISTRATION NUMBER: 29,684  
REFERENCE/DOCKET NUMBER: 12418-28  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 560 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-592-500-2

Query Match 13.5%; Score 247; DB 3; Length 560;  
Best Local Similarity 28.6%; Pred. No. 1.2e-14;  
Matches 112; Conservative 42; Mismatches 145; Indels 92; Gaps 14;

QY 7 LLAVSAQYTR--PCFPGCQC-----EVEFTGIFDSFSLTRVDCSGIG-- 48

Fri Aug 6 10:47:55 2004

us-10-017-390a-397.rapb

Page 1

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 2, 2004, 16:24:32 ; Search time 46 Seconds  
(without alignments)  
2407.176 Million cell updates/sec

Title: US-10-017-390a-397  
Perfect score: 1828  
Sequence: 1 MWPLLILAVSGAQTTRPC.....KVLHCVDRSARGPITL 353

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Gapop 10.0 , Gapext 0.5

Searched: 1291235 seqs, 313682936 residues

Total number of hits satisfying chosen parameters: 1291235

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 500 summaries

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18: /cgml\_6/prodata/2/pubppa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1828	100.0	353	10	US-09-946-374-397 Sequence 397, App
2	1828	100.0	353	12	US-10-006-485A-397 Sequence 397, App
3	1828	100.0	353	12	US-10-013-907A-397 Sequence 397, App
4	1828	100.0	353	12	US-10-015-499A-397 Sequence 397, App
5	1828	100.0	353	12	US-10-013-910A-397 Sequence 397, App
6	1828	100.0	353	12	US-10-015-495A-397 Sequence 397, App
7	1828	100.0	353	12	US-10-015-495A-397 Sequence 397, App
8	1828	100.0	353	12	US-10-006-856A-397 Sequence 397, App
9	1828	100.0	353	14	US-10-006-818A-397 Sequence 397, App
10	1828	100.0	353	14	US-10-015-393A-397 Sequence 397, App
11	1828	100.0	353	14	US-10-015-869A-397 Sequence 397, App
12	1828	100.0	353	14	US-10-012-121A-397 Sequence 397, App
13	1828	100.0	353	14	US-10-006-116A-397 Sequence 397, App
14	1828	100.0	353	14	US-10-006-117A-397 Sequence 397, App
15	1828	100.0	353	14	US-10-017-527A-397 Sequence 397, App

16	1828	100.0	353	14	US-10-013-913A-397 Sequence 397, App
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79	318.5	17.4	713	9	US-09-905-821A-245 Sequence 245, App
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86	318.5	17.4	713	10	US-09-907-613-245 Sequence 245, App
87	318.5	17.4	713	10	US-09-907-942-245 Sequence 245, App
88	318.5	17.4	713	10	US-09-904-859-245 Sequence 245, App

58	318.5	17.4	713	US-09-909-204-245	Sequence 245, App	162	276	15.1	883	15	US-10-235-027-184	Sequence 143, App
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90	318.5	17.4	713	US-09-904-786-245	Sequence 245, App	164	276	15.1	883	15	US-10-173-999-28	Sequence 28, App
91	318.5	17.4	713	US-09-906-646-245	Sequence 245, App	165	276	15.1	883	15	US-10-173-999-28	Sequence 29, App
92	318.5	17.4	713	US-09-906-646-245	Sequence 245, App	166	276	15.1	883	15	US-10-173-999-28	Sequence 30, App
93	318.5	17.4	713	US-09-906-700-245	Sequence 245, App	167	276	15.1	883	15	US-10-173-999-28	Sequence 31, App
94	318.5	17.4	713	US-09-903-786-245	Sequence 245, App	168	276	15.1	883	15	US-10-173-999-28	Sequence 32, App
95	318.5	17.4	713	US-09-903-786-245	Sequence 245, App	169	276	15.1	883	15	US-10-173-999-28	Sequence 33, App
96	318.5	17.4	713	US-09-903-786-245	Sequence 245, App	170	276	15.1	883	15	US-10-173-999-28	Sequence 34, App
97	318.5	17.4	713	US-09-904-749A-245	Sequence 245, App	171	276	15.1	883	15	US-10-173-999-28	Sequence 35, App
98	318.5	17.4	713	US-09-904-956-245	Sequence 245, App	172	276	15.1	883	15	US-10-173-999-28	Sequence 36, App
99	318.5	17.4	713	US-09-902-736-245	Sequence 245, App	173	276	15.1	883	15	US-10-173-999-28	Sequence 37, App
100	318.5	17.4	713	US-09-902-736-245	Sequence 245, App	174	276	15.1	883	15	US-10-173-999-28	Sequence 38, App
101	318.5	17.4	713	US-09-903-943-245	Sequence 245, App	175	276	15.1	883	15	US-10-173-999-28	Sequence 39, App
102	318.5	17.4	713	US-09-904-462-245	Sequence 245, App	176	276	15.1	883	15	US-10-173-999-28	Sequence 40, App
103	318.5	17.4	713	US-09-907-925-245	Sequence 245, App	177	276	15.1	883	15	US-10-173-999-28	Sequence 41, App
104	318.5	17.4	713	US-09-902-692-245	Sequence 245, App	178	276	15.1	883	15	US-10-173-999-28	Sequence 42, App
105	318.5	17.4	713	US-09-903-520-245	Sequence 245, App	179	276	15.1	883	15	US-10-173-999-28	Sequence 43, App
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107	318.5	17.4	713	US-09-909-064-245	Sequence 245, App	181	276	15.1	883	15	US-10-173-999-28	Sequence 45, App
108	318.5	17.4	713	US-09-904-553-245	Sequence 245, App	182	276	15.1	883	15	US-10-173-999-28	Sequence 46, App
109	318.5	17.4	713	US-09-905-381-245	Sequence 245, App	183	276	15.1	883	15	US-10-173-999-28	Sequence 47, App
110	318.5	17.4	713	US-09-905-088-245	Sequence 245, App	184	276	15.1	883	15	US-10-173-999-28	Sequence 48, App
111	318.5	17.4	713	US-09-907-575-245	Sequence 245, App	185	276	15.1	883	15	US-10-173-999-28	Sequence 49, App
112	318.5	17.4	713	US-09-905-075-245	Sequence 245, App	186	276	15.1	883	15	US-10-173-999-28	Sequence 50, App
113	318.5	17.4	713	US-09-902-759-245	Sequence 245, App	187	276	15.1	883	15	US-10-173-999-28	Sequence 51, App
114	318.5	17.4	713	US-09-902-634-245	Sequence 245, App	188	276	15.1	883	15	US-10-173-999-28	Sequence 52, App
115	318.5	17.4	713	US-09-902-713-245	Sequence 245, App	189	276	15.1	883	15	US-10-173-999-28	Sequence 53, App
116	318.5	17.4	713	US-09-907-979-245	Sequence 245, App	190	276	15.1	883	15	US-10-173-999-28	Sequence 54, App
117	318.5	17.4	713	US-09-902-615-245	Sequence 245, App	191	276	15.1	883	15	US-10-173-999-28	Sequence 55, App
118	318.5	17.4	713	US-09-903-925-245	Sequence 245, App	192	276	15.1	883	15	US-10-173-999-28	Sequence 56, App
119	318.5	17.4	713	US-09-906-760A-245	Sequence 245, App	193	276	15.1	883	15	US-10-173-999-28	Sequence 57, App
120	318.5	17.4	713	US-09-903-823-245	Sequence 245, App	194	276	15.1	883	15	US-10-173-999-28	Sequence 58, App
121	318.5	17.4	713	US-09-907-652-245	Sequence 245, App	195	276	15.1	883	15	US-10-173-999-28	Sequence 59, App
122	318.5	17.4	713	US-09-902-572A-245	Sequence 245, App	196	276	15.1	883	15	US-10-173-999-28	Sequence 60, App
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124	318.5	17.4	713	US-09-905-125-245	Sequence 245, App	198	276	15.1	883	15	US-10-173-999-28	Sequence 62, App
125	318.5	17.4	713	US-09-906-815A-245	Sequence 245, App	199	276	15.1	883	15	US-10-173-999-28	Sequence 63, App
126	318.5	17.4	713	US-09-905-449-245	Sequence 245, App	200	276	15.1	883	15	US-10-173-999-28	Sequence 64, App
127	318.5	17.4	713	US-09-903-806-245	Sequence 245, App	201	276	15.1	883	15	US-10-173-999-28	Sequence 65, App
128	318.5	17.4	713	US-09-904-992-245	Sequence 245, App	202	276	15.1	883	15	US-10-173-999-28	Sequence 66, App
129	318.5	17.4	713	US-09-904-838-245	Sequence 245, App	203	276	15.1	883	15	US-10-173-999-28	Sequence 67, App
130	318.5	17.4	713	US-09-906-777-245	Sequence 245, App	204	276	15.1	883	15	US-10-173-999-28	Sequence 68, App
131	318.5	17.4	713	US-09-903-603A-245	Sequence 245, App	205	276	15.1	883	15	US-10-173-999-28	Sequence 69, App
132	318.5	17.4	713	US-09-904-533-245	Sequence 245, App	206	276	15.1	883	15	US-10-173-999-28	Sequence 70, App
133	318.5	17.4	713	US-09-904-766-245	Sequence 245, App	207	276	15.1	883	15	US-10-173-999-28	Sequence 71, App
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135	318.5	17.4	713	US-09-903-562-245	Sequence 245, App	209	276	15.1	883	15	US-10-173-999-28	Sequence 73, App
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137	318.5	17.4	713	US-09-907-728-245	Sequence 245, App	211	276	15.1	883	15	US-10-173-999-28	Sequence 75, App
138	318.5	17.4	713	US-09-907-728-245	Sequence 245, App	212	276	15.1	883	15	US-10-173-999-28	Sequence 76, App
139	318.5	17.4	713	US-09-904-805-245	Sequence 245, App	213	276	15.1	883	15	US-10-173-999-28	Sequence 77, App
140	318.5	17.4	713	US-09-904-938A-245	Sequence 245, App	214	276	15.1	883	15	US-10-173-999-28	Sequence 78, App
141	318.5	17.4	713	US-09-906-722A-245	Sequence 245, App	215	276	15.1	883	15	US-10-173-999-28	Sequence 79, App
142	318.5	17.4	713	US-09-908-576-245	Sequence 245, App	216	276	15.1	883	15	US-10-173-999-28	Sequence 80, App
143	318.5	17.4	713	US-09-903-640-245	Sequence 245, App	217	276	15.1	883	15	US-10-173-999-28	Sequence 81, App
144	318.5	17.4	713	US-09-908-093-245	Sequence 245, App	218	276	15.1	883	15	US-10-173-999-28	Sequence 82, App
145	318.5	17.4	713	US-09-904-485-245	Sequence 245, App	219	276	15.1	883	15	US-10-173-999-28	Sequence 83, App
146	318.5	17.4	713	US-09-905-348-245	Sequence 245, App	220	276	15.1	883	15	US-10-173-999-28	Sequence 84, App
147	318.5	17.4	713	US-10-298-993-245	Sequence 245, App	221	276	15.1	883	15	US-10-173-999-28	Sequence 85, App
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149	318.5	17.4	713	US-10-125-166-4	Sequence 4, App1	223	276	15.1	883	15	US-10-235-027-184	Sequence 143, App
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236	267.5	14.6	673	12	US-09-989-728-52	Sequence 52, Appl	309	267.5	14.6	673	14	US-10-063-716-16	Sequence 16, Appl
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240	267.5	14.6	673	12	US-10-063-515-16	Sequence 16, Appl	313	267.5	14.6	673	14	US-10-063-726-16	Sequence 16, Appl
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245	267.5	14.6	673	12	US-10-063-555-16	Sequence 16, Appl	318	267.5	14.6	673	14	US-10-063-523-16	Sequence 16, Appl
246	267.5	14.6	673	12	US-10-063-553-16	Sequence 16, Appl	319	267.5	14.6	673	14	US-10-063-527-16	Sequence 16, Appl
247	267.5	14.6	673	12	US-10-063-594-16	Sequence 16, Appl	320	267.5	14.6	673	14	US-10-063-579-16	Sequence 16, Appl
248	267.5	14.6	673	12	US-10-063-553-16	Sequence 16, Appl	321	267.5	14.6	673	14	US-10-063-581-16	Sequence 16, Appl
249	267.5	14.6	673	12	US-10-063-554-16	Sequence 16, Appl	322	267.5	14.6	673	14	US-10-063-583-16	Sequence 16, Appl
250	267.5	14.6	673	12	US-09-997-641-52	Sequence 52, Appl	323	267.5	14.6	673	14	US-10-063-593-16	Sequence 16, Appl
251	267.5	14.6	673	12	US-09-991-150-52	Sequence 52, Appl	324	267.5	14.6	673	14	US-10-063-596-16	Sequence 16, Appl
252	267.5	14.6	673	13	US-10-063-567-16	Sequence 16, Appl	325	267.5	14.6	673	14	US-10-063-600-16	Sequence 16, Appl
253	267.5	14.6	673	13	US-10-063-567-16	Sequence 16, Appl	326	267.5	14.6	673	14	US-10-063-604-16	Sequence 16, Appl
254	267.5	14.6	673	14	US-10-063-616-16	Sequence 16, Appl	327	267.5	14.6	673	14	US-10-063-607-16	Sequence 16, Appl
255	267.5	14.6	673	14	US-10-063-502-16	Sequence 16, Appl	328	267.5	14.6	673	14	US-10-063-612-16	Sequence 16, Appl
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257	267.5	14.6	673	14	US-10-063-598-16	Sequence 16, Appl	330	267.5	14.6	673	14	US-10-063-640-16	Sequence 16, Appl
258	267.5	14.6	673	14	US-10-227-693-16	Sequence 16, Appl	331	267.5	14.6	673	14	US-10-063-652-16	Sequence 16, Appl
259	267.5	14.6	673	14	US-10-063-567-16	Sequence 16, Appl	332	267.5	14.6	673	14	US-10-063-654-16	Sequence 16, Appl
260	267.5	14.6	673	14	US-10-063-538-16	Sequence 16, Appl	333	267.5	14.6	673	14	US-10-063-659-16	Sequence 16, Appl
261	267.5	14.6	673	14	US-10-063-539-16	Sequence 16, Appl	334	267.5	14.6	673	14	US-10-063-644-16	Sequence 16, Appl
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2830P1C1  
CURRENT FILING DATE: US/09/946, 374  
CURRENT FILING DATE: 2001-09-04  
PRIOR APPLICATION NUMBER: 60/098716  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098723  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098749  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098750  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098803  
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PRIOR FILING DATE: 1998-10-07  
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PRIOR APPLICATION NUMBER: 60/105266  
PRIOR FILING DATE: 1998-10-22  
PRIOR APPLICATION NUMBER: 60/105693  
PRIOR FILING DATE: 1998-10-26  
PRIOR APPLICATION NUMBER: 60/105694  
PRIOR FILING DATE: 1998-10-26  
PRIOR APPLICATION NUMBER: 60/105807

Query Match 100.0%; Score 1828; DB 10; Length 353;  
Best Local Similarity 100.0%; Pred. No. 5, 5e-156;  
Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPWPLLLAVSAGQTRPCPCQCEVEFTFGIFDSFSLTRYDSCGSLGPHIMVPIDPT 60  
DB 1 MPWPLLLAVSAGQTRPCPCQCEVEFTFGIFDSFSLTRYDSCGSLGPHIMVPIDPT 60  
QY AHIDSSNRLEWNEVSVALGPGYTTIAGLDLSHNLITISPTAFSRLRLTESLDLSHGL 120  
DB 61 AHIDSSNRLEWNEVSVALGPGYTTIAGLDLSHNLITISPTAFSRLRLTESLDLSHGL 120  
QY 121 TALPASFTSPSPSDVNLSHNOLREVSFAFTTHSOGRLAHVDLSHNLHRLVPHPTAG 180  
DB 121 TALPASFTSPSPSDVNLSHNOLREVSFAFTTHSOGRLAHVDLSHNLHRLVPHPTAG 180  
QY 181 LPAFTIQSLNLANRRLHAAVNLRLDLPLRYLSLDGNFLAVIGGAFAGLGLTHLSLAIQ 240  
DB 181 LPAFTIQSLNLANRRLHAAVNLRLDLPLRYLSLDGNFLAVIGGAFAGLGLTHLSLAIQ 240  
QY 241 RLPELAPSGRELPGLQVLDISGNPKLNAGAEVFSGLSSLOELDLSGTLNVLPEALL 300  
DB 241 RLPELAPSGRELPGLQVLDISGNPKLNAGAEVFSGLSSLOELDLSGTLNVLPEALL 300  
QY 301 HLPALQSVSVGQDVRRCRLVREGTYPRRPGSSPKVYLHCVDTRRESAARGPTLL 353  
DB 301 HLPALQSVSVGQDVRRCRLVREGTYPRRPGSSPKVYLHCVDTRRESAARGPTLL 353

RESULT 2  
US-10-006-485A-397

; Sequence 397, Application US/10006485A  
; Publication No. US20030064062A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2830PIC9  
CURRENT APPLICATION NUMBER: US/10/006,485A  
CURRENT FILING DATE: 2001-12-06  
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PRIOR FILING DATE: 1998-10-27  
PRIOR APPLICATION NUMBER: 60/106023  
PRIOR FILING DATE: 1998-10-28

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Best Local Similarity 100.0%; Pred. No. 5.5e-156;  
Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEMPLLLIIVGGAQTTRPCFCGCOCEVETFCLEPSPSLTRVDCGLGHPVPIPIPT 60  
DB 1 MEMPLLLIIVGGAQTTRPCFCGCOCEVETFCLEPSPSLTRVDCGLGHPVPIPIPT 60  
QY 61 AHDLSSNRLKEMWNESEVLAGPGYTTLAGLDSHNLITSISPTAFSLRYLESJDSHNGL 120  
DB 61 AHDLSSNRLKEMWNESEVLAGPGYTTLAGLDSHNLITSISPTAFSLRYLESJDSHNGL 120  
QY 121 TALPASFSTSSPLSDVNSHNLREVSVAFTTHSQGRALHYDLSHNLIRLVPHPTPAG 180  
DB 121 TALPASFSTSSPLSDVNSHNLREVSVAFTTHSQGRALHYDLSHNLIRLVPHPTPAG 180  
QY 181 LPAPTIQSINLAWNRHAYPNRDLPLRYLSIDGNPLAVIGGAPAGLGLTHLSIASIQ 240  
DB 181 LPAPTIQSINLAWNRHAYPNRDLPLRYLSIDGNPLAVIGGAPAGLGLTHLSIASIQ 240  
QY 241 RLPELAPSGFRELPGLQVIDLSGNPKLNWAGAEVFSGLSSLOELDLSGTNVLVPEBALLL 300  
DB 241 RLPELAPSGFRELPGLQVIDLSGNPKLNWAGAEVFSGLSSLOELDLSGTNVLVPEBALLL 300

QY 301 HLPALQSVSVGQDVRRCRLVREGTYPRRPGSSPKVPLHCVDTRESAARGPTTL 353  
 Db 301 HLPALQSVSVGQDVRRCRLVREGTYPRRPGSSPKVPLHCVDTRESAARGPTTL 353

## RESULT 3

US-10-013-907A-397  
 ; Sequence 397, Application US/10013907A  
 ; Publication No. US20030064925A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Eaton, Dan I.  
 ; APPLICANT: Ferrera, Napoleone  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Gao, Wei-Qiang  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, Christopher J.  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Hillan, Kenneth J.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Paoni, Nicholas F.  
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 ; FILE OF INVENTION: Acids Encoding the Same  
 ; FILE REFERENCE: P2830P1C34  
 ; CURRENT APPLICATION NUMBER: US/10/013, 907A  
 ; CURRENT FILING DATE: 2001-12-10  
 ; Prior Application removed - See File Wrapper or Palm  
 ; NUMBER OF SEQ ID NOS: 477  
 ; SEQ ID NO 397  
 ; LENGTH: 353  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-10-013-907A-397

Query Match 100.0%; Score 1828; DB 12; Length 353;  
 Best Local Similarity 100.0%; Pred. No. 5.5e-156;  
 Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPWPLLLLLAVSGAQTTRPCPCGQCEVETFGLPDSFSLTRVDCSGLGPHIMVPIPLDT 60  
 Db 1 MPWPLLLLLAVSGAQTTRPCPCGQCEVETFGLPDSFSLTRVDCSGLGPHIMVPIPLDT 60  
 QY 61 AHLDLSNRLEWNEVSLAGPGYTTLAGDLSHNLTSISPTAFSLRYLESGLDSHNGL 120  
 Db 61 AHLDLSNRLEWNEVSLAGPGYTTLAGDLSHNLTSISPTAFSLRYLESGLDSHNGL 120  
 QY 121 TALPAESFTSSPLSDVNLSHNQLREVSVAFTTHSQGRALHYDLSHNLIHRLVPHPTAG 180  
 Db 121 TALPAESFTSSPLSDVNLSHNQLREVSVAFTTHSQGRALHYDLSHNLIHRLVPHPTAG 180  
 QY 181 LPAFTTOSLNLAMRHLAVPNLRDLPLRYSLDGNPLAVYGPAPFAGLGLTHLSLASIQ 240  
 Db 181 LPAFTTOSLNLAMRHLAVPNLRDLPLRYSLDGNPLAVYGPAPFAGLGLTHLSLASIQ 240  
 QY 241 RLPELAPSGRRELPGQVLDLSGNPKLWAGAEVFSGLSLOELDLSGTNLVLPPEALL 300  
 Db 241 RLPELAPSGRRELPGQVLDLSGNPKLWAGAEVFSGLSLOELDLSGTNLVLPPEALL 300  
 QY 301 HLPALQSVSVGQDVRRCRLVREGTYPRRPGSSPKVPLHCVDTRESAARGPTTL 353  
 Db 301 HLPALQSVSVGQDVRRCRLVREGTYPRRPGSSPKVPLHCVDTRESAARGPTTL 353

## RESULT 4

US-10-015-499A-397  
 ; Sequence 397, Application US/10015499A  
 ; Publication No. US20030065142A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Eaton, Dan I.  
 ; APPLICANT: Ferrera, Napoleone  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Gao, Wei-Qiang  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, Christopher J.  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Hillan, Kenneth J.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Paoni, Nicholas F.  
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 ; FILE OF INVENTION: Acids Encoding the Same  
 ; FILE REFERENCE: P2830P1C42  
 ; CURRENT APPLICATION NUMBER: US/10/015, 499A  
 ; CURRENT FILING DATE: 2001-12-11  
 ; Prior Application removed - See File Wrapper or Palm  
 ; NUMBER OF SEQ ID NOS: 477  
 ; SEQ ID NO 397  
 ; LENGTH: 353  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-10-015-499A-397

Query Match 100.0%; Score 1828; DB 12; Length 353;  
 Best Local Similarity 100.0%; Pred. No. 5.5e-156;  
 Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPWPLLLLLAVSGAQTTRPCPCGQCEVETFGLPDSFSLTRVDCSGLGPHIMVPIPLDT 60  
 Db 1 MPWPLLLLLAVSGAQTTRPCPCGQCEVETFGLPDSFSLTRVDCSGLGPHIMVPIPLDT 60  
 QY 61 AHLDLSNRLEWNEVSLAGPGYTTLAGDLSHNLTSISPTAFSLRYLESGLDSHNGL 120  
 Db 61 AHLDLSNRLEWNEVSLAGPGYTTLAGDLSHNLTSISPTAFSLRYLESGLDSHNGL 120  
 QY 121 TALPAESFTSSPLSDVNLSHNQLREVSVAFTTHSQGRALHYDLSHNLIHRLVPHPTAG 180  
 Db 121 TALPAESFTSSPLSDVNLSHNQLREVSVAFTTHSQGRALHYDLSHNLIHRLVPHPTAG 180  
 QY 181 LPAFTTOSLNLAMRHLAVPNLRDLPLRYSLDGNPLAVYGPAPFAGLGLTHLSLASIQ 240  
 Db 181 LPAFTTOSLNLAMRHLAVPNLRDLPLRYSLDGNPLAVYGPAPFAGLGLTHLSLASIQ 240  
 QY 241 RLPELAPSGRRELPGQVLDLSGNPKLWAGAEVFSGLSLOELDLSGTNLVLPPEALL 300  
 Db 241 RLPELAPSGRRELPGQVLDLSGNPKLWAGAEVFSGLSLOELDLSGTNLVLPPEALL 300  
 QY 301 HLPALQSVSVGQDVRRCRLVREGTYPRRPGSSPKVPLHCVDTRESAARGPTTL 353  
 Db 301 HLPALQSVSVGQDVRRCRLVREGTYPRRPGSSPKVPLHCVDTRESAARGPTTL 353

## RESULT 5

US-10-013-910A-397  
 ; Sequence 397, Application US/10013910A  
 ; Publication No. US20030187192A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Eaton, Dan I.  
 ; APPLICANT: Ferrera, Napoleone  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Gao, Wei-Qiang  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, Christopher J.  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Hillan, Kenneth J.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Paoni, Nicholas F.

```

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: F2830PIC33
; CURRENT APPLICATION NUMBER: US/10/013,910A
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099556
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 397
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-013-910A-397

Query Match          100.0%; Score 1828; DB 12; Length 353;
Best Local Similarity 100.0%; Pred. No. 5.5e-156;
Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPEWLLLLAVSAGQTRPCFPGCCVEFTFGLFDSFSLTRVDCSGIGPHIMPVPIPDT 60
DB 1 MPEWLLLLAVSAGQTRPCFPGCCVEFTFGLFDSFSLTRVDCSGIGPHIMPVPIPDT 60
QY 61 AHLDLSNRLEWNVESVLAAGPGYTTLAGDLSHNLTSISPTAFSRRLRYLESIDLSHNGL 120
DB 61 AHLDLSNRLEWNVESVLAAGPGYTTLAGDLSHNLTSISPTAFSRRLRYLESIDLSHNGL 120
QY 121 TALPAESFTSSPLSDVNLSHNQAREVSVAFTTHSQGRALHVDLSHNLHRLVPHPTAG 180
DB 121 TALPAESFTSSPLSDVNLSHNQAREVSVAFTTHSQGRALHVDLSHNLHRLVPHPTAG 180
QY 181 LPAPTITQSLNLAWRILAVPNLRDLPLRYLSLDGNPLAVIGGAPAGLGLTHLSIASIQ 240
DB 181 LPAPTITQSLNLAWRILAVPNLRDLPLRYLSLDGNPLAVIGGAPAGLGLTHLSIASIQ 240
QY 241 RLPELAPSGFRELPGLOVLDLSGNPKLNWAGAEVFSGLSSLOELDLSGTNLVLPPEALL 300
DB 241 RLPELAPSGFRELPGLOVLDLSGNPKLNWAGAEVFSGLSSLOELDLSGTNLVLPPEALL 300
QY 301 HLPALQSVGVQDVRCRLVREGTYPRRGSSPKVPLHCVDRRESAARGPTIL 353
DB 301 HLPALQSVGVQDVRCRLVREGTYPRRGSSPKVPLHCVDRRESAARGPTIL 353

RESULT 6
US-10-226-254A-397
; Sequence 397, Application US/10226254A
; Publication No. US20030224478A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman

```

```

; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gunney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830PIC68
; CURRENT APPLICATION NUMBER: US/10/226,254A
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 397
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-226-254A-397

Query Match          100.0%; Score 1828; DB 12; Length 353;
Best Local Similarity 100.0%; Pred. No. 5.5e-156;
Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPEWLLLLAVSAGQTRPCFPGCCVEFTFGLFDSFSLTRVDCSGIGPHIMPVPIPDT 60
DB 1 MPEWLLLLAVSAGQTRPCFPGCCVEFTFGLFDSFSLTRVDCSGIGPHIMPVPIPDT 60
QY 61 AHLDLSNRLEWNVESVLAAGPGYTTLAGDLSHNLTSISPTAFSRRLRYLESIDLSHNGL 120
DB 61 AHLDLSNRLEWNVESVLAAGPGYTTLAGDLSHNLTSISPTAFSRRLRYLESIDLSHNGL 120
QY 121 TALPAESFTSSPLSDVNLSHNQAREVSVAFTTHSQGRALHVDLSHNLHRLVPHPTAG 180
DB 121 TALPAESFTSSPLSDVNLSHNQAREVSVAFTTHSQGRALHVDLSHNLHRLVPHPTAG 180
QY 181 LPAPTITQSLNLAWRILAVPNLRDLPLRYLSLDGNPLAVIGGAPAGLGLTHLSIASIQ 240
DB 181 LPAPTITQSLNLAWRILAVPNLRDLPLRYLSLDGNPLAVIGGAPAGLGLTHLSIASIQ 240
QY 241 RLPELAPSGFRELPGLOVLDLSGNPKLNWAGAEVFSGLSSLOELDLSGTNLVLPPEALL 300
DB 241 RLPELAPSGFRELPGLOVLDLSGNPKLNWAGAEVFSGLSSLOELDLSGTNLVLPPEALL 300
QY 301 HLPALQSVGVQDVRCRLVREGTYPRRGSSPKVPLHCVDRRESAARGPTIL 353
DB 301 HLPALQSVGVQDVRCRLVREGTYPRRGSSPKVPLHCVDRRESAARGPTIL 353

RESULT 7
US-10-015-395A-397
; Sequence 397, Application US/10015395A

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; Publication No. US20040073015A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrera, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C57
; CURRENT APPLICATION NUMBER: US/10/015,395A
; CURRENT FILING DATE: 2001-12-12
; Prior Application removed - See file Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 397
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-015-395a-397

```

```

Query Match      100.0%; Score 1828; DB 12; Length 353;
Best Local Similarity 100.0%; Pred. No. 5,5e-156;
Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MPWLLLLAVSGAQTTRPCPCGCCCEVEITFGFDFSFSLTRVDCSGLGPHIMVPIPLDT 60
DB 1 MPWLLLLAVSGAQTTRPCPCGCCCEVEITFGFDFSFSLTRVDCSGLGPHIMVPIPLDT 60
QY 61 AHLDSSNRLEWNEVSVAAGPYTTLAGDLSHNLITSISPTAFSLRYLESIDLSHNGI 120
DB 61 AHLDSSNRLEWNEVSVAAGPYTTLAGDLSHNLITSISPTAFSLRYLESIDLSHNGI 120
QY 121 TALPASFTSSPLSDVNLISNOIREVSVAFTTHSGGRALHVDLSHNLHRLVPHPTTAG 180
DB 121 TALPASFTSSPLSDVNLISNOIREVSVAFTTHSGGRALHVDLSHNLHRLVPHPTTAG 180
QY 121 TALPASFTSSPLSDVNLISNOIREVSVAFTTHSGGRALHVDLSHNLHRLVPHPTTAG 180
DB 121 TALPASFTSSPLSDVNLISNOIREVSVAFTTHSGGRALHVDLSHNLHRLVPHPTTAG 180
QY 181 LPAPTIOSLNLANRRLHVAENLRLDLPLRYLSLDGNPLAVIGGAFAGLGGLTHLSLSIQ 240
DB 181 LPAPTIOSLNLANRRLHVAENLRLDLPLRYLSLDGNPLAVIGGAFAGLGGLTHLSLSIQ 240
QY 241 RLPELAPSGRRELPGQVLDLSGNPKLNWAGAVFSGLSLDELDSGNTLVLPBALLL 300
DB 241 RLPELAPSGRRELPGQVLDLSGNPKLNWAGAVFSGLSLDELDSGNTLVLPBALLL 300
QY 301 HLPALQSVSVGQDVRGRLVREGTYPRRPGSSPKVPLHCVDTRESAARGPTIL 353
DB 301 HLPALQSVSVGQDVRGRLVREGTYPRRPGSSPKVPLHCVDTRESAARGPTIL 353

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RESULT 8
US-10-006-856a-397
; Sequence 397, Application US/10006856A
; Publication No. US20030044841A1

```

```

; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrera, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.

```

```

; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C14
; CURRENT APPLICATION NUMBER: US/10/006,856A
; CURRENT FILING DATE: 2002-05-10
; NUMBER OF SEQ ID NOS: 477
; Prior Application removed - See file Wrapper or Palm
; SEQ ID NO 397
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-006-856a-397

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Query Match      100.0%; Score 1828; DB 14; Length 353;
Best Local Similarity 100.0%; Pred. No. 5,5e-156;
Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MPWLLLLAVSGAQTTRPCPCGCCCEVEITFGFDFSFSLTRVDCSGLGPHIMVPIPLDT 60
DB 1 MPWLLLLAVSGAQTTRPCPCGCCCEVEITFGFDFSFSLTRVDCSGLGPHIMVPIPLDT 60
QY 61 AHLDSSNRLEWNEVSVAAGPYTTLAGDLSHNLITSISPTAFSLRYLESIDLSHNGI 120
DB 61 AHLDSSNRLEWNEVSVAAGPYTTLAGDLSHNLITSISPTAFSLRYLESIDLSHNGI 120
QY 121 TALPASFTSSPLSDVNLISNOIREVSVAFTTHSGGRALHVDLSHNLHRLVPHPTTAG 180
DB 121 TALPASFTSSPLSDVNLISNOIREVSVAFTTHSGGRALHVDLSHNLHRLVPHPTTAG 180
QY 121 TALPASFTSSPLSDVNLISNOIREVSVAFTTHSGGRALHVDLSHNLHRLVPHPTTAG 180
DB 121 TALPASFTSSPLSDVNLISNOIREVSVAFTTHSGGRALHVDLSHNLHRLVPHPTTAG 180
QY 181 LPAPTIOSLNLANRRLHVAENLRLDLPLRYLSLDGNPLAVIGGAFAGLGGLTHLSLSIQ 240
DB 181 LPAPTIOSLNLANRRLHVAENLRLDLPLRYLSLDGNPLAVIGGAFAGLGGLTHLSLSIQ 240
QY 241 RLPELAPSGRRELPGQVLDLSGNPKLNWAGAVFSGLSLDELDSGNTLVLPBALLL 300
DB 241 RLPELAPSGRRELPGQVLDLSGNPKLNWAGAVFSGLSLDELDSGNTLVLPBALLL 300
QY 301 HLPALQSVSVGQDVRGRLVREGTYPRRPGSSPKVPLHCVDTRESAARGPTIL 353
DB 301 HLPALQSVSVGQDVRGRLVREGTYPRRPGSSPKVPLHCVDTRESAARGPTIL 353

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RESULT 9
US-10-006-818a-397

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```

; Sequence 397, Application US/10006818A
; Publication No. US20030054406A1

```

```

; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrera, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C4
; CURRENT APPLICATION NUMBER: US/10/006,818A
; CURRENT FILING DATE: 2001-12-06
; Prior Application removed - See file Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 397

```

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; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-006-818A-397

Query Match          100.0%; Score 1828; DB 14; Length 353;
Best Local Similarity 100.0%; Pred. No. 5.5e-156;
Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MWPULLLLIAVSGAQTTRPCFCGCGCEVETFGLEFDSFSLTRVDCSGLGPHIMVPPIPLDT 60
DB 1 MWPULLLLIAVSGAQTTRPCFCGCGCEVETFGLEFDSFSLTRVDCSGLGPHIMVPPIPLDT 60

QY 61 AHHDLSSNRLEWNEVSVLAPGYTTLAGLDLSHNLITSSIPAFSLRYLESIDLSSHNGL 120
DB 61 AHHDLSSNRLEWNEVSVLAPGYTTLAGLDLSHNLITSSIPAFSLRYLESIDLSSHNGL 120

QY 121 TALPAESFTSSPLSDVNLSHNQLREVSVSAFTTHSQGRALHVDLSHNLHRLVPHPTTAG 180
DB 121 TALPAESFTSSPLSDVNLSHNQLREVSVSAFTTHSQGRALHVDLSHNLHRLVPHPTTAG 180

QY 181 LPAPTIOGLNLAWRHLAVPNLRDLPLRYLSLDGNPLAVIPGAPFAGLGGLTHLSLSAQ 240
DB 181 LPAPTIOGLNLAWRHLAVPNLRDLPLRYLSLDGNPLAVIPGAPFAGLGGLTHLSLSAQ 240

QY 241 RLPELAPSGFRELPGLQVLDLSGNPKLNWAGAEVFSGLSIOELDLSGTNLVPLPEALL 300
DB 241 RLPELAPSGFRELPGLQVLDLSGNPKLNWAGAEVFSGLSIOELDLSGTNLVPLPEALL 300

QY 301 HLPALQSVSVGQDVRCRLVREGTYPRRPGSSPKVPLHCVDTRESAARGPTIL 353
DB 301 HLPALQSVSVGQDVRCRLVREGTYPRRPGSSPKVPLHCVDTRESAARGPTIL 353

RESULT 10
US-10-015-393A-397
; Sequence 397, Application US/10015393A
; Publication No. US20030069179A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Baton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C46
; CURRENT APPLICATION NUMBER: US/10/015,393A
; PRIOR APPLICATION REMOVED - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 397
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-015-393A-397

Query Match          100.0%; Score 1828; DB 14; Length 353;
Best Local Similarity 100.0%; Pred. No. 5.5e-156;
Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MWPULLLLIAVSGAQTTRPCFCGCGCEVETFGLEFDSFSLTRVDCSGLGPHIMVPPIPLDT 60
DB 1 MWPULLLLIAVSGAQTTRPCFCGCGCEVETFGLEFDSFSLTRVDCSGLGPHIMVPPIPLDT 60
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```

QY 61 AHHDLSSNRLEWNEVSVLAPGYTTLAGLDLSHNLITSSIPAFSLRYLESIDLSSHNGL 120
DB 61 AHHDLSSNRLEWNEVSVLAPGYTTLAGLDLSHNLITSSIPAFSLRYLESIDLSSHNGL 120

QY 121 TALPAESFTSSPLSDVNLSHNQLREVSVSAFTTHSQGRALHVDLSHNLHRLVPHPTTAG 180
DB 121 TALPAESFTSSPLSDVNLSHNQLREVSVSAFTTHSQGRALHVDLSHNLHRLVPHPTTAG 180

QY 181 LPAPTIOGLNLAWRHLAVPNLRDLPLRYLSLDGNPLAVIPGAPFAGLGGLTHLSLSAQ 240
DB 181 LPAPTIOGLNLAWRHLAVPNLRDLPLRYLSLDGNPLAVIPGAPFAGLGGLTHLSLSAQ 240

QY 241 RLPELAPSGFRELPGLQVLDLSGNPKLNWAGAEVFSGLSIOELDLSGTNLVPLPEALL 300
DB 241 RLPELAPSGFRELPGLQVLDLSGNPKLNWAGAEVFSGLSIOELDLSGTNLVPLPEALL 300

QY 301 HLPALQSVSVGQDVRCRLVREGTYPRRPGSSPKVPLHCVDTRESAARGPTIL 353
DB 301 HLPALQSVSVGQDVRCRLVREGTYPRRPGSSPKVPLHCVDTRESAARGPTIL 353

RESULT 11
US-10-015-869A-397
; Sequence 397, Application US/10015869A
; Publication No. US20030073130A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Baton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C45
; CURRENT APPLICATION NUMBER: US/10/015,869A
; PRIOR APPLICATION REMOVED - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 397
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-015-869A-397

Query Match          100.0%; Score 1828; DB 14; Length 353;
Best Local Similarity 100.0%; Pred. No. 5.5e-156;
Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MWPULLLLIAVSGAQTTRPCFCGCGCEVETFGLEFDSFSLTRVDCSGLGPHIMVPPIPLDT 60
DB 1 MWPULLLLIAVSGAQTTRPCFCGCGCEVETFGLEFDSFSLTRVDCSGLGPHIMVPPIPLDT 60

QY 61 AHHDLSSNRLEWNEVSVLAPGYTTLAGLDLSHNLITSSIPAFSLRYLESIDLSSHNGL 120
DB 61 AHHDLSSNRLEWNEVSVLAPGYTTLAGLDLSHNLITSSIPAFSLRYLESIDLSSHNGL 120

QY 121 TALPAESFTSSPLSDVNLSHNQLREVSVSAFTTHSQGRALHVDLSHNLHRLVPHPTTAG 180
DB 121 TALPAESFTSSPLSDVNLSHNQLREVSVSAFTTHSQGRALHVDLSHNLHRLVPHPTTAG 180

QY 181 LPAPTIOGLNLAWRHLAVPNLRDLPLRYLSLDGNPLAVIPGAPFAGLGGLTHLSLSAQ 240
DB 181 LPAPTIOGLNLAWRHLAVPNLRDLPLRYLSLDGNPLAVIPGAPFAGLGGLTHLSLSAQ 240
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QY 241 RLPELAPSGFREIPGIVDLDISGNPKLNAGAEVFSGLSLOELDLSGNNLVPLEALL 300  
DB 241 RLPELAPSGFREIPGIVDLDISGNPKLNAGAEVFSGLSLOELDLSGNNLVPLEALL 300  
QY 301 HLPALQSVGVGVRCRLVREGTYRRRPGSSPKYPLHCVDTRRESAARGPTLL 353  
DB 301 HLPALQSVGVGVRCRLVREGTYRRRPGSSPKYPLHCVDTRRESAARGPTLL 353

RESULT 12  
US-10-012-121A-397  
; Sequence 397, Application US/10012121A  
; Publication No.: US20030073810A1  
GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan I.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2830P1C20  
CURRENT APPLICATION NUMBER: US/10/012,121A  
CURRENT FILING DATE: 2001-12-07  
Prior Application removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 477  
SEQ ID NO 397  
LENGTH: 353  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-012-121A-397

Query Match 100.0%; Score 1828; DB 14; Length 353;  
Best Local Similarity 100.0%; Pred No. 5.5e-156;  
Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPWPLLLAVSGAQTTRPCPGCCQCEVEFTFGIFDSFLTRYDCSGLGPHIMPVPIPLDT 60  
DB 1 MPWPLLLAVSGAQTTRPCPGCCQCEVEFTFGIFDSFLTRYDCSGLGPHIMPVPIPLDT 60  
QY 61 AHDDLSNRLKEMNEBVLAGPGVTLTLAGLDLSHNLITLSPFAFSRLRLTESLDSHNL 120  
DB 61 AHDDLSNRLKEMNEBVLAGPGVTLTLAGLDLSHNLITLSPFAFSRLRLTESLDSHNL 120  
QY 121 TALPASFTSSPLSDVNLSHNQLREVSVAFTTHSGRALHYDLSHNLTHRLVPHPTAG 180  
DB 121 TALPASFTSSPLSDVNLSHNQLREVSVAFTTHSGRALHYDLSHNLTHRLVPHPTAG 180  
QY 181 LPAPTTQSLNLANRRLHAYPNLFDLPLRLYSLDGNPLAYTGCAFPAGGLGTHLSLSIQ 240  
DB 181 LPAPTTQSLNLANRRLHAYPNLFDLPLRLYSLDGNPLAYTGCAFPAGGLGTHLSLSIQ 240  
QY 241 RLPELAPSGFREIPGIVDLDISGNPKLNAGAEVFSGLSLOELDLSGNNLVPLEALL 300  
DB 241 RLPELAPSGFREIPGIVDLDISGNPKLNAGAEVFSGLSLOELDLSGNNLVPLEALL 300  
QY 301 HLPALQSVGVGVRCRLVREGTYRRRPGSSPKYPLHCVDTRRESAARGPTLL 353  
DB 301 HLPALQSVGVGVRCRLVREGTYRRRPGSSPKYPLHCVDTRRESAARGPTLL 353

RESULT 13  
US-10-006-116A-397

; Sequence 397, Application US/10006116A  
; Publication No.: US20030082626A1  
GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan I.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2830P1C15  
CURRENT APPLICATION NUMBER: US/10/006,116A  
CURRENT FILING DATE: 2001-12-16  
PRIOR APPLICATION NUMBER: 60/058716  
PRIOR FILING DATE: 1998-09-01  
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PRIOR FILING DATE: 1998-09-16  
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PRIOR FILING DATE: 1998-09-16  
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PRIOR FILING DATE: 1998-10-28

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Matches 333; Conservative 0; Mismatches 0;

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DB 1 MPMPLLLILAVSAGQOTTRPCFPCCCEVEYFGLPDSFSLTRVDCGSLGPHIMVPIPIDT 60  
QY 61 AHDLSNRLEVNNSVLAGPGYTLGIDLSHNLTISPTAFRLRLBSLDSHGL 120  
DB 61 AHDLSNRLEVNNSVLAGPGYTLGIDLSHNLTISPTAFRLRLBSLDSHGL 120  
QY 121 TALPASFSSPLSDVNLSHNLREVSVAPFTTHSQGRALHVDLSHNLHRLVPHPTBAG 180  
DB 121 TALPASFSSPLSDVNLSHNLREVSVAPFTTHSQGRALHVDLSHNLHRLVPHPTBAG 180  
QY 181 LPAPTQSLNLMNRKLAHVENDJPLRYLSLDGNPLAVIGGAGAGGGLTHLSLASIQ 240  
DB 181 LPAPTQSLNLMNRKLAHVENDJPLRYLSLDGNPLAVIGGAGAGGGLTHLSLASIQ 240



Db 181 LPAPTQSLNLANRHLHAVNRLDLRLRYSLDGNPLAVIGPAGAGLGLTHLSLSLQ 240  
Qy 241 RLPFLAPSGFRELPGIQTVDLSGNPKLNAGAEVSGSLSDLELDLSGNINVLPEALL 300  
Db 241 RLPFLAPSGFRELPGIQTVDLSGNPKLNAGAEVSGSLSDLELDLSGNINVLPEALL 300  
Qy 301 HLPALQSVGVGDVRCRLVREGTYPRRPGSSPKYPLHCVDTRESAARGPTIL 353  
Db 301 HLPALQSVGVGDVRCRLVREGTYPRRPGSSPKYPLHCVDTRESAARGPTIL 353

RESULT 14  
US-10-006-117A-397  
; Sequence 397, Application US/10006117A  
; Publication No. US20030082627A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan 1.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2830P1C13  
; CURRENT APPLICATION NUMBER: US/10/006,117A  
; PRIOR FILING DATE: 2002-03-19  
; PRIOR APPLICATION removed - See File Wrapper or Palm  
; PRIOR FILING DATE: 2001-07-09  
; NUMBER OF SEQ ID NOS: 477  
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; ORGANISM: Homo sapiens  
US-10-006-117A-397

Query Match 100.0%; Score 1828; DB 14; Length 353;  
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Matches 353; Conservative 0; Mismatches 0;

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Qy 61 AHDLSNRIEMNESVLAGPGYTTLAGLDLSHNLITSISPTAFSLRLYLSLDSHNGL 120  
Db 61 AHDLSNRIEMNESVLAGPGYTTLAGLDLSHNLITSISPTAFSLRLYLSLDSHNGL 120  
Qy 121 TALPASFTSSPLSDVNLISNOLREVSAFTTHSGRLHYDLSNHLHRLVPHPTAG 180  
Db 121 TALPASFTSSPLSDVNLISNOLREVSAFTTHSGRLHYDLSNHLHRLVPHPTAG 180  
Qy 181 LPAPTQSLNLANRHLHAVNRLDLRLRYSLDGNPLAVIGPAGAGLGLTHLSLSLQ 240  
Db 181 LPAPTQSLNLANRHLHAVNRLDLRLRYSLDGNPLAVIGPAGAGLGLTHLSLSLQ 240  
Qy 241 RLPFLAPSGFRELPGIQTVDLSGNPKLNAGAEVSGSLSDLELDLSGNINVLPEALL 300  
Db 241 RLPFLAPSGFRELPGIQTVDLSGNPKLNAGAEVSGSLSDLELDLSGNINVLPEALL 300  
Qy 301 HLPALQSVGVGDVRCRLVREGTYPRRPGSSPKYPLHCVDTRESAARGPTIL 353  
Db 301 HLPALQSVGVGDVRCRLVREGTYPRRPGSSPKYPLHCVDTRESAARGPTIL 353

RESULT 15  
US-10-017-527A-397  
; Sequence 397, Application US/10017527A  
; Publication No. US20030082626A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan 1.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2830P1C63  
; CURRENT APPLICATION NUMBER: US/10/017,527A  
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Best Local Similarity	100.0%	Pred. No. 5.5e-156;		
Matches 353;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

  

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121	TALPAESFTSSPLSDVNLSHNQLREVSVSAFTTHSQGRALHVDLSHNLIHRLVLPHPTRAG	180
121	TALPAESFTSSPLSDVNLSHNQLREVSVSAFTTHSQGRALHVDLSHNLIHRLVLPHPTRAG	180

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Qy	181	LPAPTIOSLNLAWNRIHVPNIRDLPLRYLSLDGNPLAVIGGAFAGLGGTHLSLASLQ	240
Db	181	LPAPTIOSLNLAWNRIHVPNIRDLPLRYLSLDGNPLAVIGGAFAGLGGTHLSLASLQ	240
Qy	241	RLPELAPSGFRELPGLOVLDLSGNPKLNWAGAEVFGSLSSLOELDLSGTNLVPLPEALLL	300
Db	241	RLPELAPSGFRELPGLOVLDLSGNPKLNWAGAEVFGSLSSLOELDLSGTNLVPLPEALLL	300
Qy	301	HLPALQSVSVGQDVRCRRIVREGTYPRRPGSSPKVPLHCVDTRESAARGPTIL	353
Db	301	HLPALQSVSVGQDVRCRRIVREGTYPRRPGSSPKVPLHCVDTRESAARGPTIL	353

Search completed: August 2, 2004, 16:27:27  
Job time : 49 secs

GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: August 2, 2004, 16:04:02 ; Search time 13 Seconds

(without alignments)  
1413.905 Million cell updates/sec

Title: US-10-017-390A-397

Perfect score: 1828

Sequence: 1 MPWPLLLLLAVSGAQTTPC.....KVPLHCVDRBSAARGPTIL 353

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database : SwissProt\_42.1\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	313.5	17.1	713	1	GAMP_HUMAN
2	279.5	15.3	662	1	GARP_HUMAN
3	265	14.5	907	1	LGR5_HUMAN
4	257	14.1	907	1	LGR5_MOUSE
5	257	14.1	951	1	LGR4_HUMAN
6	256	14.0	951	1	LGR4_RAT
7	248	13.6	347	1	A2GL_HUMAN
8	247	13.5	560	1	GPV_HUMAN
9	240	13.1	578	1	LR15_RAT
10	239.5	13.1	567	1	GPV_RAT
11	238.5	13.0	379	1	ASPN_HUMAN
12	238	13.0	905	1	TLR3_MOUSE
13	234.5	12.8	605	1	ALS_FAPHA
14	232	12.7	373	1	ASPN_MOUSE
15	227	12.4	581	1	LR15_HUMAN
16	224.5	12.3	605	1	ALS_HUMAN
17	224	12.3	1529	1	SLR2_HUMAN
18	221.5	12.1	828	1	LGR6_HUMAN
19	220.5	12.1	782	1	CHAO_TRICA
20	220.5	12.1	904	1	TLR3_HUMAN
21	218.5	12.0	1032	1	TLR9_HUMAN
22	218	11.9	567	1	GPV_MOUSE
23	215.5	11.8	603	1	ALS_RAT
24	214.5	11.7	603	1	ALS_MOUSE
25	212	11.6	357	1	PGS2_CHICK
26	211.5	11.6	1256	1	FLII_DROME
27	209	11.4	356	1	PGS2_COTJA
28	207.5	11.4	733	1	CT75_MOUSE
29	205.5	11.2	481	1	NYX_HUMAN
30	204	11.2	582	1	SHO2_MOUSE
31	203	11.1	582	1	SHO2_HUMAN
32	199	10.9	338	1	LUM_HUMAN
33	198.5	10.9	360	1	PGS2_PIG

34	198.5	10.9	473	1	RT4R_HUMAN
35	198	10.8	354	1	PGS2_RAT
36	197	10.8	476	1	NYX_MOUSE
37	197	10.8	536	1	CBP8_HUMAN
38	197	10.8	1315	1	CHAO_DROME
39	196.5	10.7	360	1	PGS2_SHEEP
40	195.5	10.7	360	1	PGS2_BOVIN
41	195.5	10.7	360	1	PGS2_RABIT
42	195.5	10.7	740	1	CT75_HUMAN
43	194.5	10.6	354	1	PGS2_MOUSE
44	194	10.6	858	1	TLR5_HUMAN
45	193.5	10.6	342	1	LUM_BOVIN
46	192.5	10.5	360	1	PGS2_HORSE
47	191.5	10.5	1024	1	POPC_RALSO
48	191	10.4	1504	1	SLIT_DROME
49	190.5	10.4	359	1	PGS2_HUMAN
50	190.5	10.4	473	1	RT4R_MACFA
51	190.5	10.4	1032	1	TLR9_MOUSE
52	188.5	10.3	338	1	LUM_MOUSE
53	188.5	10.3	369	1	PGS1_BOVIN
54	187	10.2	360	1	PGS2_CANFA
55	187	10.2	372	1	PGS1_HORSE
56	186	10.2	754	1	LGR8_HUMAN
57	185.5	10.1	343	1	LUM_COTJA
58	184.5	10.1	331	1	PLI5_AKBL
59	183.5	10.0	338	1	LUM_RAT
60	183.5	10.0	369	1	PGS1_MOUSE
61	183.5	10.0	369	1	PGS1_RAT
62	182.5	10.0	369	1	PGS1_CANFA
63	182.5	10.0	369	1	PGS1_SHEEP
64	181.5	9.9	343	1	LUM_CHICK
65	181	9.9	496	1	TMM_ARATH
66	181	9.9	859	1	TLR5_MOUSE
67	180.5	9.9	440	1	OMGP_MOUSE
68	180	9.8	368	1	PGS1_HUMAN
69	180	9.8	1269	1	FLIH_HUMAN
70	179.5	9.8	440	1	OMGP_HUMAN
71	179.5	9.8	473	1	RT4R_MOUSE
72	179	9.8	1039	1	YR71_CABEL
73	177.5	9.7	368	1	PGS1_XENIA
74	177.5	9.7	649	1	FLR3_HUMAN
75	176	9.6	376	1	FMOD_RAT
76	176	9.6	1257	1	FLIH_CABEL
77	175	9.6	378	1	PRLP_MOUSE
78	175	9.6	473	1	RT4R_RAT
79	173.5	9.5	1032	1	TLR8_MOUSE
80	172	9.4	361	1	CHAD_BOVIN
81	172	9.4	376	1	FMOD_MOUSE
82	171.5	9.4	626	1	GPBA_HUMAN
83	171.5	9.4	682	1	CONN_DROME
84	171	9.4	375	1	FMOD_BOVIN
85	171	9.4	376	1	FMOD_HUMAN
86	170	9.3	358	1	CHAD_RAT
87	169	9.2	358	1	CHAD_MOUSE
88	167	9.1	423	1	OMD_RAT
89	167	9.1	851	1	NUDI_YEAST
90	165.5	9.1	359	1	CHAD_HUMAN
91	165.5	9.1	1115	1	GPCR_LYMS
92	165	9.0	2493	1	CYAA_USTMA
93	164.5	9.0	757	1	LGR7_HUMAN
94	164.5	9.0	2300	1	CYAA_NEUCR
95	163	8.9	699	1	ECM2_HUMAN
96	163	8.9	737	1	LGR8_MOUSE
97	163	8.9	1839	1	CYAA_SACKL
98	162.5	8.9	646	1	FLR1_HUMAN
99	162	8.9	377	1	PRLP_RAT
100	162	8.9	2026	1	CYAA_YEAST
101	161	8.8	1041	1	TLR8_HUMAN
102	160	8.7	839	1	TLR4_HUMAN
103	159.5	8.7	192	1	LUM_RABIT
104	159	8.7	382	1	PRLP_HUMAN
105	159	8.7	839	1	TLR4_PANPA
106	158	8.6	1097	1	TOLL_DROME

Q9bzt6	homo sapien
Q01129	rattus norv
P83503	mus musculus
P22792	homo sapien
P20244	drosofila
Q9tt62	ovis aries
P21793	bos taurus
Q8wt88	oryctolagus
Q28848	homo sapien
P28654	mus musculus
O60602	homo sapien
Q05443	bos taurus
Q46542	equus caball
Q9r822	raistonia s
P24014	drosofila
P07518	homo sapien
Q3n0a3	macaca fasc
Q9eq03	mus musculus
P51885	mus musculus
P21809	bos taurus
Q29393	canis fami
Q46403	equus caball
Q8wx40	homo sapien
Q9de67	coturnix co
O93233	agkistrodon
P51886	rattus norv
P28653	mus musculus
P47853	rattus norv
O02678	canis fami
Q46390	ovis aries
P51890	gallus gall
Q38641	arabidopsis
Q9j1f7	mus musculus
Q63912	mus musculus
P21810	homo sapien
Q13045	homo sapien
P23515	homo sapien
Q99pi8	mus musculus
Q09544	caenorhabdi
Q9ib75	xenopus lae
P50609	rattus norv
P34268	caenorhabdi
Q9jks3	mus musculus
Q99m75	rattus norv
P58692	mus musculus
Q27972	bos taurus
P50608	mus musculus
P07359	homo sapien
Q01819	drosofila
P13605	bos taurus
Q06828	homo sapien
Q52266	mus musculus
Q92167	rattus norv
P23336	saccharomyc
O15335	homo sapien
P46023	lymaea sta
P49606	ustilago ma
Q9bxb9	homo sapien
Q1631	neurospora
Q94769	homo sapien
Q91225	mus musculus
P23466	saccharomyc
Q9nzul	homo sapien
Q9eqp5	rattus norv
P08678	saccharomyc
Q9nr57	homo sapien
O00206	homo sapien
O46379	oryctolagus
P51888	homo sapien
Q9ttt0	pan paniscu
P08953	drosofila

107	158	1192	1	EXS ARATH	Q91yn8 arabidopsis	180	126	6.9	299	1	MIME_BOVIN	P19879 bos taurus
108	157.5	8.6	257	1	LR3 MOUSE	P59034 mus musculus	181	125.5	373	1	CD14_BOVIN	Q95122 bos taurus
109	157.5	8.6	1049	1	TLR7_HUMAN	Q9nyk1 homo sapien	182	125.5	687	1	FSHR_EQUAS	Q95179 equus asinu
110	157	8.6	272	1	PGS1_PIG	Q9gkq6 sus scrofa	183	125.5	810	1	LR8_HUMAN	Q81wt6 homo sapien
111	157	8.6	623	1	PALP_HUMAN	Q9p2v4 homo sapien	184	125.5	925	1	GLHR_ATEL	P35409 anthopleura
112	157	8.6	661	1	C180_MOUSE	Q92192 mus musculus	185	124.5	938	1	SD22_YEAST	P36047 saccharomyc
113	157	8.6	833	1	TLR4_FELCA	P58127 felis silve	186	124.5	938	1	LR8_MOUSE	Q80wg5 mus musculus
114	155.5	8.5	380	1	FMOD_CHICK	P51887 gallus gall	187	123	784	1	TLR2_CRIGR	Q80lfe cricetus
115	155.5	8.5	843	1	TLR4_HORSE	Q9myw3 equus cabal	188	122.5	784	1	LR3_HUMAN	Q9by71 homo sapien
116	155	8.5	1207	1	BR11_LYCP	Q81899 lycopersico	189	122.5	795	1	TLR2_MOUSE	Q9epw9 mus musculus
117	154	8.4	381	1	PRLP_BOVIN	Q8kn8 bos taurus	190	122	795	1	TLR6_MOUSE	P33543 arabidopsis
118	154	8.4	1207	1	BR11_LYCS	Q8qud5 lycopersico	191	121.5	674	1	TL1_ARATH	Q920a0 mus musculus
119	152.5	8.3	257	1	LR3 FAT	P59035 rattus norv	192	121	328	1	OPT_MOUSE	Q8k1s1 mus musculus
120	152	8.3	841	1	TLR4_BOVIN	Q9g165 bos taurus	193	121	630	1	IG14_MOUSE	P23799 trypanosoma
121	151.5	8.3	423	1	OMD_MOUSE	O35103 mus musculus	194	120.5	630	1	ESR8_HYBB	Q8k1s1 mus musculus
122	151.5	8.3	826	1	TLR4_PAPAN	Q9tsp2 papio anubi	195	120	694	1	FSHR_HORSE	P47799 equus cabal
123	150.5	8.2	977	1	Y848_HUMAN	O94933 homo sapien	196	119	694	1	CD14_RAT	Q63691 rattus norv
124	150.5	8.2	1050	1	TLR7_MOUSE	P58681 mus musculus	197	118	793	1	TL21_CHICK	Q9dd78 gallus gall
125	150	8.2	326	1	YN29_CABEL	P45969 caenorhabdi	198	117.5	784	1	TLR2_BOVIN	Q951a9 bos taurus
126	148.5	8.1	793	1	CD11_HUMAN	Q9y219 homo sapien	199	116.5	64	1	GP1X_HUMAN	P14770 homo sapien
127	148	8.1	835	1	TLR4_MOUSE	Q9quk6 mus musculus	200	116	330	1	PG11_ARATH	Q9m519 arabidopsis
128	148	8.1	966	1	Y918_HUMAN	O94991 homo sapien	201	115.5	63	1	YDDK_SHEEP	P76123 escherichia
129	147	8.0	351	1	KERA_MOUSE	O35367 mus musculus	202	115.5	63	1	FSHR_SHEEP	P35379 ovias aries
130	147	8.0	800	1	INLA_LISMO	P25146 listeria mo	203	115.5	942	1	TMK1_ARATH	P43298 arabidopsis
131	145	7.9	838	1	TLR4_CRIGR	Q9wv82 cricetus	204	114	366	1	CD14_MOUSE	P12259 homo sapien
132	145	7.9	1196	1	BR11_ARATH	O22476 arabidopsis	205	114	224	1	PA5_HUMAN	P55456 rhizobium s
133	144.5	7.9	327	1	OPT CANFA	P83286 canis famli	206	113.5	62	1	Y4FR_RHSN	Q8epq1 mus musculus
134	144.5	7.9	375	1	CD14_HUMAN	P08571 homo sapien	207	113.5	62	1	TLR1_MOUSE	Q8vab8 mus musculus
135	143	7.8	298	1	MIME_MOUSE	Q62000 mus musculus	208	113	518	1	LR2_MOUSE	P39337 saccharomyc
136	143	7.8	332	1	OPT_HUMAN	Q9ubm4 homo sapien	209	113	630	1	PAC2_YEAST	P20395 rattus norv
137	142.5	7.8	147	1	FMOD_RABIT	O46378 cryptolagus	210	112.5	62	1	FSHR_RAT	Q9m518 arabidopsis
138	142.5	7.8	294	1	MIME_CHICK	Q9w6ho gallus gall	211	112.5	62	1	PG12_ARATH	P26337 trypanosoma
139	142.5	7.8	2145	1	CYAA_PODAN	O41513 podospira a	212	112.5	630	1	ESR8_TRYEO	Q9y2c9 homo sapien
140	142	7.8	352	1	KERA_BOVIN	O62702 bos taurus	213	112	62	1	TLR6_HUMAN	P24786 sus scrofa
141	142	7.8	1692	1	CYAA_SCHPO	P14605 schizosacch	214	111.5	825	1	TRK2_PIG	Q16288 homo sapien
142	141.5	7.7	293	1	MIME_COTJA	Q9de65 coturnix co	215	111	839	1	TRK2_HUMAN	P35376 bos taurus
143	141.5	7.7	321	1	PGLE_BOVIN	P79119 bos taurus	216	110.5	695	1	FSHR_BOVIN	Q09299 caenorhabdi
144	141.5	7.7	617	1	PALP_RAT	Q9imh2 rattus norv	217	110	699	1	YQOA_CABEL	P13608 bos taurus
145	141	7.7	322	1	PGLE_HUMAN	Q9g645 homo sapien	218	109.5	60	1	PGCA_BOVIN	P14763 canis famli
146	140.5	7.7	322	1	LUM_PIG	Q9tcb4 sus scrofa	219	109	764	1	TSHR CANFA	Q9syq8 arabidopsis
147	140.5	7.7	353	1	KERA_CHICK	O42235 gallus gall	220	109	980	1	CLV1_ARATH	P35378 mus musculus
148	140.5	7.7	781	1	KERA_COTJA	Q9de66 coturnix co	221	108.5	62	1	FSHR_MOUSE	Q63604 rattus norv
149	140.5	7.7	781	1	TL22_CHICK	Q9dgb6 gallus gall	222	108.5	5.9	821	TRK2_RAT	Q91rr4 arabidopsis
150	140	7.7	618	1	PALP_MOUSE	Q8k099 mus musculus	223	108.5	5.9	1054	R131_ARATH	P47750 mus musculus
151	139.5	7.6	414	1	LLR1_HUMAN	Q96150 homo sapien	224	108	764	1	TSHR_MOUSE	Q9by88 homo sapien
152	138.5	7.6	421	1	OMD_HUMAN	Q99983 homo sapien	225	107.5	5.9	371	LR2_HUMAN	Q15399 homo sapien
153	138	7.5	322	1	PGLE_MOUSE	P70186 mus musculus	226	107	2944	1	TLR1_HUMAN	P22194 schizosacch
154	137	7.5	409	1	YOPM_YERPE	P17778 yersinia pe	227	106.5	5.8	786	SD22_SCHPO	P32112 macaca fasc
155	136	7.4	352	1	KERA_HUMAN	O60938 homo sapien	228	105	332	1	FSHR_MACFA	P21463 rattus norv
156	136	7.4	999	1	RLK5_ARATH	P47735 arabidopsis	229	104.5	5.7	695	TRK2_RAT	Q08874 mus musculus
157	135.5	7.4	342	1	PG13_PHAVU	P58823 phaseolus v	230	104.5	5.7	764	MITF_MOUSE	P23945 homo sapien
158	135.5	7.4	537	1	LG14_HUMAN	Q8n135 homo sapien	231	104.5	5.7	864	PGIP_PYRGO	Q05091 pyrus commu
159	135	7.4	316	1	PGLE_CHICK	Q90944 gallus gall	232	104	526	1	LSHR_SHEEP	Q28585 ovias aries
160	135	7.4	372	1	D100_ARATH	Q00874 arabidopsis	233	104	526	1	TSHR_BOVIN	Q27987 bos taurus
161	134	7.3	4303	1	PKD1_HUMAN	P98161 homo sapien	234	103.5	5.7	763	NOR2_ALCEU	Q9k4u8 alcaligenes
162	133	7.3	784	1	TLR2 MACFA	Q95m53 macaca fasc	235	103.5	5.6	521	MITF_HUMAN	Q75030 homo sapien
163	132	7.2	422	1	OMD_BOVIN	O77742 bos taurus	236	103	526	1	BAK1_ARATH	Q94f62 arabidopsis
164	131.5	7.2	835	1	TLR4 RAT	Q9qx05 rattus norv	237	103	526	1	FSHR_PIG	P49059 sus scrofa
165	131.5	7.2	1021	1	PSK2 DAUCA	Q8lpb4 daucus caro	238	103	526	1	MITF_HUMAN	P24449 zea mays (m
166	131	7.2	548	1	LG13_MOUSE	Q8k406 mus musculus	239	102.5	5.6	615	FSHR_PIG	Q94f62 arabidopsis
167	130.5	7.1	276	1	RSU1_HUMAN	Q15404 homo sapien	240	102.5	5.6	695	ZEAC MAIZE	P24449 zea mays (m
168	130	7.1	372	1	CD14_RABIT	Q28680 cryptolagus	241	102	5.6	774	RFNC_PSEAE	Q9bxb8 pseudomonas
169	129.5	7.1	342	1	PG11_PHAVU	P35334 phaseolus v	242	102	5.6	259	LP15_MOUSE	Q96pb8 homo sapien
170	129	7.1	276	1	RSU1_MOUSE	Q01730 mus musculus	243	101.5	5.6	259	LR15_MOUSE	Q8vch9 mus musculus
171	129	7.1	661	1	C180_HUMAN	Q99467 homo sapien	244	101.5	5.6	827	TRK2_CHICK	Q91044 gallus gall
172	129	7.1	784	1	TLR2_HUMAN	O60603 homo sapien	245	100	5.5	135	PGS1_RABIT	Q46377 cryptolagus
173	128.5	7.0	574	1	IP4A_SHIFL	P18009 shigella fl	246	100	5.5	811	TLR4_HUMAN	Q9bxb8 pseudomonas
174	128.5	7.0	660	1	FLR2_HUMAN	O43155 homo sapien	247	100	5.5	811	Y014_HUMAN	Q96pb8 homo sapien
175	127.5	7.0	548	1	LG13_HUMAN	Q8n145 homo sapien	248	99.5	5.4	493	TRKA_CHICK	Q15048 homo sapien
176	127	6.9	298	1	MIME_HUMAN	P20774 homo sapien	249	99.5	5.4	778	PMAB_ARATH	Q91009 gallus gall
177	127	6.9	1008	1	PSKR_ARATH	Q9zvr7 arabidopsis	250	99.5	5.4	956	BIRB_MOUSE	Q91v11 arabidopsis
178	126.5	6.9	342	1	PG12_PHAVU	P58822 phaseolus v	251	99	5.4	1447	LG11_HUMAN	Q9guk4 mus musculus
179	126.5	6.9	545	1	LG12_HUMAN	Q8n0v4 homo sapien	252	98	5.4	557		Q95970 homo sapien

253	98	5.4	557	1	LG11 MOUSE	Q9jial mus musculus	326	88.5	4.8	234	1	ZEAL MAIZE	P02859 zea mays (m
254	98	5.4	557	1	LG11 RAT	Q9k4y5 rattus norv	327	88.5	4.8	338	1	PO43 HUMAN	Q15319 homo sapien
255	98	5.4	764	1	TSKR SHEEP	P56495 ovis aries	328	88.5	4.8	386	1	RN1 SCHPO	P41391 schizosacch
256	98	5.4	821	1	TKB MOUSE	P15209 mus musculus	329	88.5	4.8	855	1	MUTS PSEAE	Q9hy08 pseudomonas
257	97.5	5.3	773	1	YOD3 CAEEL	P34595 caenorhabdi	330	88	4.8	206	1	GPBB HUMAN	P13224 homo sapien
258	97	5.3	456	1	RINI PIG	P10775 sus scrofa	331	88	4.8	928	1	BCS3 HUMAN	Q9h6u6 homo sapien
259	97	5.3	693	1	FSHR CHICK	P79763 gallus gall	332	88	4.8	957	1	PM1 NICPL	Q08435 nicotiana p
260	97	5.3	701	1	LSHR BOVIN	Q28005 bos taurus	333	88	4.8	1114	1	RET HUMAN	P07949 homo sapien
261	97	5.3	764	1	TSKR HUMAN	P16473 homo sapien	334	88	4.8	1115	1	FRPA NEIMC	P55126 neisseria m
262	97	5.3	928	1	BCS3 MOUSE	Q8ccn5 mus musculus	335	88	4.8	1829	1	FRPC NEIMC	P55127 neisseria m
263	96.5	5.3	532	1	IP47 SHIFL	P18014 shigella fl	336	88	4.8	2167	1	SHK1 RAT	Q9w448 rattus norv
264	96.5	5.3	794	1	TRK1 LYNST	Q76997 lymphaea sta	337	88	4.8	2415	1	PGCA HUMAN	P16112 homo sapien
265	96	5.3	263	1	ZEAX MAIZE	P04700 zea mays (m	338	88	4.8	2936	1	NBEA MOUSE	Q9epn1 mus musculus
266	96	5.3	266	1	ZEAX MAIZE	P04699 zea mays (m	339	87.5	4.8	234	1	ZEAX MAIZE	P06675 zea mays (m
267	96	5.3	1258	1	GLI2 HUMAN	P10070 homo sapien	340	87.5	4.8	466	1	VL2 HPV52	P36763 human papil
268	95.5	5.2	630	1	INLB LISMO	P25147 listeria mo	341	87.5	4.8	847	1	R133 ARATH	Q9ste7 arabidopsis
269	95.5	5.2	1027	1	AF10 HUMAN	P55197 homo sapien	342	87.5	4.8	1251	1	YM11 YEAST	Q04545 saccharomyc
270	95.5	5.2	1329	1	KF10 HUMAN	Q9p218 homo sapien	343	87.5	4.8	2594	1	7LES DROVI	P20806 drosophila
271	95	5.2	463	1	DNAA PROMP	Q95487 prochloroco	344	87	4.8	659	1	DNAA CHLAB	Q8gh79 chlamydomo
272	95	5.2	593	1	FRZF MYXCA	P17559 myxococcus	345	87	4.8	662	1	GGT4 MOUSE	Q991p7 mus musculus
273	95	5.2	799	1	ZY11 CAEEL	P21541 caenorhabdi	346	87	4.8	699	1	LSHR HUMAN	P22888 homo sapien
274	95	5.2	818	1	TRKB CHICK	Q91987 gallus gall	347	86.5	4.7	1040	1	CARF HUMAN	Q9hc29 homo sapien
275	95	5.2	822	1	TRKB HUMAN	Q16620 homo sapien	348	86.5	4.7	1093	1	NA14 HUMAN	Q86w24 homo sapien
276	95	5.2	901	1	Y298 HUMAN	Q15016 homo sapien	349	86.5	4.7	1155	1	C1HB BACTM	Q45718 bacillus th
277	94.5	5.2	511	1	AL21 SCHPO	Q10303 schizosacch	350	86.5	4.7	2333	1	PGCA CANFA	Q28343 canis fami
278	94.5	5.2	1093	1	AF17 HUMAN	P55198 homo sapien	351	86.5	4.7	2432	1	Y43R TRV6	P18305 chilo iride
279	94	5.1	339	1	FABH STRLI	Q9f6d4 streptomyce	352	86.5	4.7	3341	1	POLG MCFA	P33615 m genome po
280	94	5.1	799	1	TRKA RAT	P35739 rattus norv	353	86	4.7	398	1	DXR SALTI	Q829a6 salmonella
281	94	5.1	2258	1	FA5 PIG	Q9glp1 sus scrofa	354	86	4.7	483	1	CTDB HUMAN	Q9h579 homo sapien
282	94	5.1	2717	1	ZEP1 HUMAN	P15822 homo sapien	355	86	4.7	513	1	NORI ALCEU	Q9k4v0 alcaligenes
283	93.5	5.1	677	1	LX1B MOUSE	Q95936 mus musculus	356	86	4.7	556	1	PLD STRAT	Q53728 streptomyce
284	93.5	5.1	1378	1	WPS2 ARATH	Q9fh83 arabidopsis	357	86	4.7	926	1	SC24 YEAST	P40482 saccharomyc
285	93	5.1	617	1	SH2 MOUSE	Q9jia7 mus musculus	358	86	4.7	982	1	CLB8 HUMAN	Q13191 homo sapien
286	92.5	5.1	567	1	PGTA HUMAN	Q92696 homo sapien	359	86	4.7	1157	1	RPOB TROW8	P59642 tropheryma
287	92.5	5.1	837	1	CCR4 YEAST	P31384 saccharomyc	360	86	4.7	1157	1	RPOB TROWT	Q95662 tropheryma
288	92.5	5.1	1115	1	TBC2 CHLRE	Q8vxp3 chlamydomon	361	86	4.7	2161	1	SHK1 HUMAN	Q9y566 homo sapien
289	92.5	5.1	1776	1	POLR OVYV	P20127 ononis yell	362	86	4.7	2161	1	SHK1 HUMAN	P24450 zea mays (m
290	92	5.0	402	1	PGK CHLPN	Q927m5 chlamydia p	363	85.5	4.7	233	1	ZEAD MAIZE	Q63955 mus musculus
291	92	5.0	435	1	CREA BOTCI	Q94130 botrytis ci	364	85.5	4.7	338	1	PO43 MOUSE	P74155 synchocyst
292	92	5.0	481	1	GLNA HELPU	Q921w5 helicobacte	365	85.5	4.7	384	1	OXAA SYN3	Q9h1b4 homo sapien
293	92	5.0	539	1	FXL6 HUMAN	Q8h531 homo sapien	366	85.5	4.7	397	1	NXFS HUMAN	Q9ub9 homo sapien
294	92	5.0	1230	1	UGS4 SOLTU	Q43846 solanum tub	367	85.5	4.7	619	1	NXFI HUMAN	P16582 sus scrofa
295	92	5.0	1372	1	WR16 ARATH	Q9f192 arabidopsis	368	85.5	4.7	696	1	LSHR PIG	Q70494 mus musculus
296	92	5.0	3144	1	VP13 YEAST	Q07878 saccharomyc	369	85.5	4.7	725	1	SP3 MOUSE	O42484 arabidopsis
297	91.5	5.0	267	1	ZEAX MAIZE	P04698 zea mays (m	370	85.5	4.7	909	1	CCAG RAT	O54898 rattus norv
298	91.5	5.0	460	1	VATB THEVO	Q97cp9 thermoplas	371	85.5	4.7	2254	1	GPBB MOUSE	P56400 mus musculus
299	91	5.0	331	1	YB52 SYN3	P74221 synchocyst	372	85	4.6	206	1	MOAT PSEAE	Q9h3d6 pseudomonas
300	91	5.0	625	1	GCKR HUMAN	Q14397 homo sapien	373	85	4.6	329	1	TERM AD540	P48313 human adeno
301	91	5.0	781	1	SP3 HUMAN	Q02447 homo sapien	374	85	4.6	646	1	TR2N AGRVI	P25017 agrobacteri
302	91	5.0	960	1	PM44 ARATH	Q9su58 arabidopsis	375	85	4.6	755	1	YFHM ECOLI	P76578 escherichia
303	91	5.0	1736	1	CAB2 MOUSE	P64739 mus musculus	376	85	4.6	1653	1	GALL PASMU	P27899 pasteurella
304	90.5	5.0	267	1	KAP2 SCORBI	P14691 sorghum bic	377	84.5	4.6	385	1	POLG HCVJ2	Q43950 azotobacter
305	90.5	5.0	469	1	MURD AGRIS	Q8udm6 agrobacteri	378	84.5	4.6	776	1	HYPE AZOCH	P57959 hepatitis c
306	90.5	5.0	567	1	PGTA MOUSE	Q9jhk4 mus musculus	379	84.5	4.6	788	1	BCSE XANAC	Q43950 xanthomonas
307	90.5	5.0	567	1	PGTA RAT	Q08602 rattus norv	380	84.5	4.6	1895	1	WR19 ARATH	Q9s277 arabidopsis
308	90.5	5.0	852	1	R134 ARATH	Q38834 arabidopsis	381	84.5	4.6	2426	1	SON HUMAN	P18583 homo sapien
309	90.5	5.0	5147	1	FAT DRCPY	P33450 drosophila	382	84.5	4.6	267	1	ZEAL MAIZE	P04701 zea mays (m
310	90	4.9	208	1	GPBB PAPCY	Q04785 papio cynoc	383	84	4.6	337	1	PLSX VIBMA	Q9a35 vibrio mari
311	90	4.9	232	1	TRPF LIPST	Q01128 lipomyces s	384	84	4.6	359	1	KLFB HUMAN	Q95600 homo sapien
312	90	4.9	662	1	GGT4 RAT	Q9sm74 rattus norv	385	84	4.6	481	1	GLNA HELPY	P94845 helicobacte
313	90	4.9	675	1	HS7M PHAVU	Q01899 phaseolus v	386	84	4.6	538	1	KL11 YEAST	P23291 saccharomyc
314	90	4.9	676	1	LSHR CALJA	P02721 callithrix	387	84	4.6	580	1	MP12 HUMAN	P30305 homo sapien
315	90	4.9	796	1	TRKA HUMAN	P04629 homo sapien	388	84	4.6	677	1	TKT1 CANAL	O17323 caenorhabdi
316	90	4.9	1302	1	FRPA NEIMB	Q9k0k9 neisseria m	389	84	4.6	816	1	HDA7 CAEEL	P49657 drosophila
317	90	4.9	1829	1	FRPC NEIMC	Q91yv5 neisseria m	390	84	4.6	843	1	MNB DRONE	O64483 arabidopsis
318	89.5	4.9	225	1	GIBB THETH	Q91cy2 thermus the	391	84	4.6	876	1	SIRK ARATH	P59594 arabidopsis
319	89.5	4.9	607	1	YN92 YEAST	P53749 saccharomyc	392	84	4.6	910	1	RP8H ARATH	P07898 gallus gall
320	89.5	4.9	1025	1	DPD2 PIG	Q28943 sus scrofa	393	84	4.6	2109	1	PGCA CHICK	Q35516 mus musculus
321	89	4.9	261	1	ZEAX MAIZE	P06679 zea mays (m	394	84	4.6	2470	1	NCT2 MOUSE	P78559 homo sapien
322	89	4.9	538	1	YFUL ECOLI	P52127 escherichia	395	84	4.6	2805	1	MAPA HUMAN	O83828 treponema p
323	89	4.9	1142	1	GINA YEAST	Q12263 saccharomyc	396	83.5	4.6	325	1	Y856 TREPA	P28810 pseudomonas
324	89	4.9	3707	1	PGBM MOUSE	Q05793 mus musculus	397	83.5	4.6	496	1	MMSA_PSEAE	
325	89	4.9	3969	1	HRX HUMAN	Q03164 homo sapien	398	83.5	4.6				

399	83.5	4.6	576	1	SLP1 CAEL	P34260	caenorhabdi	472	80.5	4.4	477	1	LPC3 HUMAN	P59926	homo sapien
400	83.5	4.6	789	1	ATX1 RAT	Q63540	rattus norv	473	80.5	4.4	523	1	SRC RSVPA	P31693	rous sarcom
401	83.5	4.6	928	1	KRL1 YEAST	P36003	saccharomyc	474	80.5	4.4	621	1	ILV5 MYCAV	Q59498	mycobacteri
402	83.5	4.6	1162	1	FXL6 HUMAN	Q92k27	homo sapien	475	80.5	4.4	720	1	GT11 SCHPO	O14367	schizosacch
403	83.5	4.6	1204	1	ATY2 HUMAN	Q9nd20	homo sapien	476	80.5	4.4	781	1	YB68 SCHPO	Q09748	schizosacch
404	83.5	4.6	1592	1	YNY2 YEAST	P53855	saccharomyc	477	80.5	4.4	811	1	PRIA RHORU	P05445	rhodospiril
405	83.5	4.6	2531	1	NTC1 MOUSE	Q01705	mus musculus	478	80.5	4.4	855	1	CLOC MOUSE	O08785	mus musculus
406	83	4.6	2531	1	YNY2 YEAST	P06674	zea mays (m	479	80.5	4.4	855	1	MUTS AZOVI	P27345	azotobacter
407	83	4.5	344	1	RPOA SPIXK	Q98462	spirogyra m	480	80.5	4.4	941	1	MSH1 SCHPO	O75385	homo sapien
408	83	4.5	419	1	GLPB ECOLI	P13033	escherichia	481	80.5	4.4	1050	1	ULK1 HUMAN	O54826	mus musculus
409	83	4.5	424	1	SRF2 HUMAN	Q13309	homo sapien	482	80.5	4.4	1068	1	AF10 MOUSE	P79621	mus musculus
410	83	4.5	504	1	ARL2 AGRT5	Q8u705	agrobacteri	483	80.5	4.4	1155	1	C2TA MOUSE	O62190	mus musculus
411	83	4.5	535	1	SRC HUMAN	P12931	homo sapien	484	80.5	4.4	1378	1	ARH8 HUMAN	C15085	homo sapien
412	83	4.5	555	1	FORA ECOLI	Q47208	escherichia	485	80.5	4.4	1522	1	7LES DROME	P13368	drosophila
413	83	4.5	624	1	STS MOUSE	P50427	mus musculus	486	80.5	4.4	2554	1	TENX HUMAN	P22105	homo sapien
414	83	4.5	625	1	GLMS SYNEL	Q8dj16	s glucosami	487	80.5	4.4	4289	1	A32B HUMAN	Q92688	homo sapien
415	83	4.5	682	1	H87M SOLTU	Q08276	solanum tub	488	80	4.4	251	1	HEM3 XANCP	Q8p536	xanthomonas
416	83	4.5	816	1	NP22 MOUSE	P97460	mus musculus	489	80	4.4	304	1	THIL ECOLI	P77785	escherichia
417	83	4.5	836	1	VG26 BPML5	Q05233	mycobacteri	490	80	4.4	325	1	ASSY MYCLE	Q8ccl0	mycobacteri
418	83	4.5	2124	1	PGCA RAT	P07897	rattus norv	491	80	4.4	399	1	DXR PSEPK	Q8enn4	pseudomonas
419	82.5	4.5	326	1	TPO RAT	P49745	rattus norv	492	80	4.4	400	1	SKP2 MOUSE	Q92023	mus musculus
420	82.5	4.5	445	1	YB55 MYCTU	Q50680	mycobacteri	493	80	4.4	424	1	HRA4 HUMAN	P83105	homo sapien
421	82.5	4.5	550	1	LG12 MOUSE	Q8k420	mus musculus	494	80	4.4	476	1	LAC4 THACU	Q02081	thanatephor
422	82.5	4.5	585	1	DCP3 ORYSA	P51849	oryza sativ	495	80	4.4	531	1	V70K OYMU	P20130	ononis vell
423	82.5	4.5	622	1	FACG HUMAN	O15287	homo sapien	496	80	4.4	597	1	YE45 SCHPO	O13965	schizosacch
424	82.5	4.5	628	1	HNFA MOUSE	P22361	mus musculus	497	80	4.4	730	1	YE45 SCHPO	O35643	mus musculus
425	82.5	4.5	628	1	HNFA RAT	P15257	rattus norv	498	80	4.4	943	1	ALB1 MOUSE	O74501	schizosacch
426	82.5	4.5	638	1	TOXA PSEAE	P11439	pseudomonas	499	80	4.4	1150	1	YC14 SCHPO	Q94422	homo sapien
427	82.5	4.5	651	1	PIA1 MOUSE	O88907	mus musculus	500	80	4.4	1342	1	Z335 HUMAN		
428	82.5	4.5	824	1	NP22 HUMAN	Q99743	homo sapien								
429	82.5	4.5	1024	1	SZSL HUMAN	Q9byh1	homo sapien								
430	82.5	4.5	1033	1	CIS1 MOUSE	Q8r4b8	mus musculus								
431	82	4.5	304	1	HEM3 XANAC	Q8ppr3	xanthomonas								
432	82	4.5	376	1	ACT7 ORYSA	P17300	oryza sativ								
433	82	4.5	417	1	O85E DROME	P81924	drosophila								
434	82	4.5	437	1	FLHF PSEPU	O52256	pseudomonas								
435	82	4.5	510	1	HUTH STIAU	Q93tx3	stigmatella								
436	82	4.5	535	1	FXL6 MOUSE	Q9qkx0	mus musculus								
437	82	4.5	540	1	SRC MOUSE	P05480	mus musculus								
438	82	4.5	666	1	GGT4 HUMAN	Q9uj14	homo sapien								
439	82	4.5	1035	1	MT10 YEAST	P39692	saccharomyc								
440	82	4.5	1099	1	PLC1 CANAL	O13433	candida alb								
441	82	4.5	1762	1	DPOO HUMAN	O75417	homo sapien								
442	81.5	4.5	278	1	PSTB BACHD	Q9k815	bacillus ha								
443	81.5	4.5	378	1	SUCF THERH	P25126	thermus the								
444	81.5	4.5	458	1	BPIL THEAC	Q8n4f0	homo sapien								
445	81.5	4.5	460	1	VATB THEAC	P31594	porphyra pu								
446	81.5	4.5	590	1	ILVB PORPU	Q55774	synecocyst								
447	81.5	4.5	661	1	Y182 SYN3	P11420	drosophila								
448	81.5	4.5	710	1	DA DROME	P11420	drosophila								
449	81.5	4.5	830	1	J1P2 MOUSE	Q9ere9	mus musculus								
450	81.5	4.5	885	1	AR56 SCHPO	P11318	s argl1 pro								
451	81.5	4.5	1070	1	RPOB SP1OL	P11703	spinacia ol								
452	81.5	4.5	1200	1	AT12 MOUSE	Q9epe9	mus musculus								
453	81.5	4.5	1204	1	POL MLVFF	P26810	friend muri								
454	81.5	4.5	1204	1	POL MLVFF	P26809	friend muri								
455	81.5	4.5	1204	1	MSH6 SCHPO	P26808	friend muri								
456	81.5	4.5	1254	1	PSH6 SCHPO	O74502	schizosacch								
457	81.5	4.5	5065	1	EPPL HUMAN	P58107	homo sapien								
458	81	4.4	235	1	ZE22 MAIZE	P04704	zea mays (m								
459	81	4.4	295	1	YMO3 ERWST	Q52118	erwinia ste								
460	81	4.4	306	1	PRMA XANAC	Q8pp06	xanthomonas								
461	81	4.4	377	1	ACTC ARATH	P53497	arabidopsis								
462	81	4.4	397	1	PGTC SALTU	P37591	salmonella								
463	81	4.4	413	1	COBL PSEDE	P21921	pseudomonas								
464	81	4.4	455	1	K132 HUMAN	P43630	homo sapien								
465	81	4.4	456	1	RINI RAT	P29315	rattus norv								
466	81	4.4	460	1	RINI HUMAN	P13489	homo sapien								
467	81	4.4	664	1	DNAK CHLCV	Q824b2	chlamydomphi								
468	81	4.4	700	1	LSHR RAT	P16235	rattus norv								
469	81	4.4	704	1	PM2 LYCES	P23980	lycopersico								
470	81	4.4	784	1	OSTA SALTU	Q829j6	salmonella								
471	81	4.4	2471	1	NTC2 RAT	Q9cqw30	rattus norv								

## ALIGNMENTS

RESULT 1	GAMP HUMAN	STANDARD;	PRT;	713 AA.
ID	GAMP HUMAN			
AC	O75325;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DE	10-OCT-2003 (Rel. 42, Last annotation update)			
DR	Gloma amplified on chromosome 1 protein precursor.			
GN	GAC1.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	SEQUENCE FROM N.A.			
RP	TISSUE=Glial tumor;			
RC	MEDLINE=98324709; PubMed=9662332;			
RA	Malfoy B., Almeida A., Zhu X.X., Vogt N., Tyagi R., Muleris M.,			
RA	Dutrillaux A.-M., Dutrillaux B., Ross D., Hanash S.;			
RT	"GAC1, a new member of the leucine-rich repeat superfamily on			
RT	chromosome band 1q32., is amplified and overexpressed in malignant			
RT	gliomas.";			
RL	Oncogene 16:2997-3002(1998).			
CC	-I- SUBCELLULAR LOCATION: Type I membrane protein (Potential).			
CC	-I- TISSUE SPECIFICITY: OVERAMPLIFIED IN MALIGNANT GLIOMAS.			
CC	-I- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.			
CC	-I- SIMILARITY: Contains 11 leucine-rich (LRR) repeats.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
DR	EMBL; AF030435; AAC39792.1; -			
DR	MIN; 605492; -			
DR	GO; GO:0004872; Fireceptor activity; TAS.			

DR GO; GO:0007155; P:cell adhesion; TAS.  
DR GO; GO:0007185; P:signal transduction; TAS.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003598; IG\_c2.  
DR InterPro; IPR001611; LRR.  
DR InterPro; IPR000483; LRR\_Cterm.  
DR InterPro; IPR000372; LRR\_Nterm.  
DR InterPro; IPR003591; LRR\_Typ.  
DR Pfam; PF00047; IG; 1.  
DR Pfam; PF00560; LRR; 9.  
DR PRINTS; PR001463; LRRCT; 1.  
DR PRINTS; PR00019; LEURICHRPT.  
DR SMART; SM00408; IGC2; 1.  
DR SMART; SM00369; IGC2; 1.  
DR SMART; SM00082; LRRCT; 1.  
DR SMART; SM00033; LRRNT; 1.  
DR PROSITE; PS00835; IG-LIKE; 1.  
KW Immunoglobulin domain; Transmembrane; Glycoprotein; Repeat;  
KW Leucine-rich repeat; Signal.  
FT SIGNAL 1 18  
FT CHAIN 19 713  
FT DOMAIN 19 630  
FT TRANSMEM 631 651  
FT DOMAIN 652 713  
FT REPEAT 92 115  
FT REPEAT 116 139  
FT REPEAT 140 163  
FT REPEAT 165 187  
FT REPEAT 188 211  
FT REPEAT 213 235  
FT REPEAT 236 259  
FT REPEAT 261 283  
FT REPEAT 309 333  
FT REPEAT 334 357  
FT REPEAT 359 385  
FT DOMAIN 422 511  
FT DISULFID 445 497  
FT CARBOHYD 94 94  
FT CARBOHYD 381 381  
FT CARBOHYD 555 555  
FT CARBOHYD 583 583  
SQ SEQUENCE 713 AA; 78798 MW; EC8BC0FD240C9396 CRC64;  
Query Match 17.1%; Score 313.5; DB 1; Length 713;  
Best Local Similarity 27.4%; Pred. No. 2.2e-15;  
Matches 114; Conservative 55; Mismatches 162; Indels 85; Gaps 11;  
QY 6 LILLAVSQAQT-----RPFPGCCQCEVTFGLFDSF--SLTRVDCSGLGPHMPVPI 56  
DB 8 LLLAWAGATAAPVVPVPHVCPFCQACQIRPWYTPRSSYREATVDCNDLFLTAVPAL 67  
QY 57 PLDTAHLDSNRLNEMVNESVLGPGY-TTLAGLDLSNLLTSISPTAFSLRYLESJDL 115  
DB 68 PAGTQTLLQNSIVRVQSEL---GYLANLTLDLSQNSFSDARDCCDFHALPQLLSLH 124  
QY 116 SHNGTALPASFST-SPLSDNLSHNLREVSVAFTTHSQGRALHVDLSNLIHRLVP 174  
DB 125 BENQUTREDISFAGLASLOELYLNHNOQYRIAPAFGLSNLRLH--LNSNLRAL-- 180  
QY 175 HPTAGLGPAPTQSINLAWNLHAY-----PNLRDL----- 205  
DB 181 -DSRFWEMLPNLEILMIGNKVDAILDMNFRPLANRLSLVLGMNLRISDYALEGLQSL 239  
QY 206 -----PRLYSLDGNPLAVIGPGAPAGLGGITLHSLASLQRLP 243  
DB 240 ELSFYDNLQARVPRRALEQVPLGLDLNKNPQVPGDFPANMLHKEGLNNNEELV 299  
QY 244 ELAPSGFRELPGQLVLDLSGNPKLNWAGAEVFSGLSLQELDSLSTNIVLPPEALLHL 303  
DB 300 SIDKALVNLPELTKLDITNNPRLSFTHPRAPHLPQMETLMLNNALSALHQQTVESLP 359  
QY 304 ALOQSVV-GQDVRCRLRV-----EGTYPFRPGSSPKVPLHCVDTRE 344  
GO; GO:0007155; P:cell adhesion; TAS.  
GO; GO:0007185; P:signal transduction; TAS.  
InterPro; IPR007110; IG-like.  
InterPro; IPR003598; IG\_c2.  
InterPro; IPR001611; LRR.  
InterPro; IPR000483; LRR\_Cterm.  
InterPro; IPR000372; LRR\_Nterm.  
InterPro; IPR003591; LRR\_Typ.  
Pfam; PF00047; IG; 1.  
Pfam; PF00560; LRR; 9.  
PRINTS; PR001463; LRRCT; 1.  
PRINTS; PR00019; LEURICHRPT.  
SMART; SM00408; IGC2; 1.  
SMART; SM00369; IGC2; 1.  
SMART; SM00082; LRRCT; 1.  
SMART; SM00033; LRRNT; 1.  
PROSITE; PS00835; IG-LIKE; 1.  
KW Immunoglobulin domain; Transmembrane; Glycoprotein; Repeat;  
KW Leucine-rich repeat; Signal.  
SIGNAL 1 18  
CHAIN 19 713  
DOMAIN 19 630  
TRANSMEM 631 651  
DOMAIN 652 713  
REPEAT 92 115  
REPEAT 116 139  
REPEAT 140 163  
REPEAT 165 187  
REPEAT 188 211  
REPEAT 213 235  
REPEAT 236 259  
REPEAT 261 283  
REPEAT 309 333  
REPEAT 334 357  
REPEAT 359 385  
DOMAIN 422 511  
DISULFID 445 497  
CARBOHYD 94 94  
CARBOHYD 381 381  
CARBOHYD 555 555  
CARBOHYD 583 583  
SEQUENCE 713 AA; 78798 MW; EC8BC0FD240C9396 CRC64;  
EMBL; Z24680; CAA80847.1; -;  
PIR; S42799; S42799.  
Gene; HGNC:4161; GARP.  
MIM; 137207; -;  
GO; GO:0005887; C:integral to plasma membrane; TAS.  
InterPro; IPR001611; LRR.  
InterPro; IPR000372; LRR\_Nterm.  
InterPro; IPR003591; LRR\_Typ.  
Pfam; PF00560; LRR; 15.  
PRINTS; PR001462; LRRNT; 1.  
PRINTS; PR00019; LEURICHRPT.  
SMART; SM00369; LRR\_Typ; 2.  
SMART; SM00013; LRRNT; 1.  
KW Glycoprotein; Leucine-rich repeat; Repeat; Transmembrane; Signal.  
SIGNAL 1 19  
CHAIN 20 662  
DOMAIN 20 627  
TRANSMEM 628 648  
DOMAIN 649 662  
REPEAT 8 31  
REPEAT 48 71  
REPEAT 72 95  
REPEAT 97 122  
REPEAT 123 147  
REPEAT 148 171  
REPEAT 172 195  
REPEAT 197 217  
REPEAT 218 240  
REPEAT 242 264  
REPEAT 265 286  
REPEAT 314 337  
REPEAT 339 361  
REPEAT 362 385  
REPEAT 386 408  
REPEAT 410 432  
REPEAT 442 465  
REPEAT 467 488  
REPEAT 490 513  
GO; GO:0007155; P:cell adhesion; TAS.  
GO; GO:0007185; P:signal transduction; TAS.  
InterPro; IPR007110; IG-like.  
InterPro; IPR003598; IG\_c2.  
InterPro; IPR001611; LRR.  
InterPro; IPR000483; LRR\_Cterm.  
InterPro; IPR000372; LRR\_Nterm.  
InterPro; IPR003591; LRR\_Typ.  
Pfam; PF00047; IG; 1.  
Pfam; PF00560; LRR; 9.  
PRINTS; PR001463; LRRCT; 1.  
PRINTS; PR00019; LEURICHRPT.  
SMART; SM00408; IGC2; 1.  
SMART; SM00369; IGC2; 1.  
SMART; SM00082; LRRCT; 1.  
SMART; SM00033; LRRNT; 1.  
PROSITE; PS00835; IG-LIKE; 1.  
KW Immunoglobulin domain; Transmembrane; Glycoprotein; Repeat;  
KW Leucine-rich repeat; Signal.  
SIGNAL 1 18  
CHAIN 19 713  
DOMAIN 19 630  
TRANSMEM 631 651  
DOMAIN 652 713  
REPEAT 92 115  
REPEAT 116 139  
REPEAT 140 163  
REPEAT 165 187  
REPEAT 188 211  
REPEAT 213 235  
REPEAT 236 259  
REPEAT 261 283  
REPEAT 309 333  
REPEAT 334 357  
REPEAT 359 385  
DOMAIN 422 511  
DISULFID 445 497  
CARBOHYD 94 94  
CARBOHYD 381 381  
CARBOHYD 555 555  
CARBOHYD 583 583  
SEQUENCE 713 AA; 78798 MW; EC8BC0FD240C9396 CRC64;  
EMBL; Z24680; CAA80847.1; -;  
PIR; S42799; S42799.  
Gene; HGNC:4161; GARP.  
MIM; 137207; -;  
GO; GO:0005887; C:integral to plasma membrane; TAS.  
InterPro; IPR001611; LRR.  
InterPro; IPR000372; LRR\_Nterm.  
InterPro; IPR003591; LRR\_Typ.  
Pfam; PF00560; LRR; 15.  
PRINTS; PR001462; LRRNT; 1.  
PRINTS; PR00019; LEURICHRPT.  
SMART; SM00369; LRR\_Typ; 2.  
SMART; SM00013; LRRNT; 1.  
KW Glycoprotein; Leucine-rich repeat; Repeat; Transmembrane; Signal.  
SIGNAL 1 19  
CHAIN 20 662  
DOMAIN 20 627  
TRANSMEM 628 648  
DOMAIN 649 662  
REPEAT 8 31  
REPEAT 48 71  
REPEAT 72 95  
REPEAT 97 122  
REPEAT 123 147  
REPEAT 148 171  
REPEAT 172 195  
REPEAT 197 217  
REPEAT 218 240  
REPEAT 242 264  
REPEAT 265 286  
REPEAT 314 337  
REPEAT 339 361  
REPEAT 362 385  
REPEAT 386 408  
REPEAT 410 432  
REPEAT 442 465  
REPEAT 467 488  
REPEAT 490 513





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FT REPEAT 257 279 LRR 9.
FT REPEAT 281 303 LRR 10.
FT REPEAT 304 327 LRR 11.
FT REPEAT 328 350 LRR 12.
FT REPEAT 351 375 LRR 13.
FT REPEAT 377 396 LRR 14.
FT REPEAT 397 420 LRR 15.
FT REPEAT 422 444 LRR 16.
FT REPEAT 444 464 LRR 17.
FT REPEAT 464 485 LRR 18.
FT CARBOHYD 63 63 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 63 63 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 77 77 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 208 208 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 500 500 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 792 792 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 90 90 R -> H (IN REF. 2).
FT CONFLICT 212 212 L -> W (IN REF. 2).
SQ SEQUENCE 907 AA; 99997 MW; 8225C5E6FD9092 CRC64;

Query Match 14.5%; Score 265; DB 1; Length 907;
Best Local Similarity 30.1%; Pred. No. 1e-11;
Matches 93; Conservative 32; Mismatches 102; Indels 82; Gaps 9;

QY 4 PILLLLAVSQAQ-----TTRCFPGCQCEVTFGLFDSFSLTRVDCSGLGPHIMPVPIPL 58
DB 13. PVLLQLATGSGSPRSGVLLRGCTHCEP-----DGRMLLRVDCSGLGSELPSNLSV 66

QY 59 DTAHLDSNRLNEMWESVLAGPGVTTLAGLDSHNLITSPTAFGRRLRYLESIDLDSHN 118
DB 67 FTSYLDLSNN-----ISQLPNPLSRLFELESLRAGN 100

QY 119 GLTALPAESFTS-SPLSDVNLSHNQLREVSVSAFTTHSQGRALHVDLSHNLHRLVPHPT 177
DB 101 ALTYPKGAFGLYSLKVLMLQNNLRHV-----PT 131

QY 178 RAGLPAPTIQSINLAWNLHAFVNLRLDP-----LRYLSLDQCNPLAVPGCAFAGLG 229
DB 132 BALQNLRLSLQSLRDANHSIYVP-----PSCFSGLSRLHRLWLDNDAITEIPVQAFRLS 186

QY 230 GITHLSLASLQRLAPLAPSGFRELPGQLVLDLGNPKLNWAGAEVFGSLSSLOELDLSGT 289
DB 187 ALQAMTLA-LNKIHIPDYAFGNLSLVVHLHNN-RHLSKKGKCFGLHSLETLIDLNNY 244

QY 290 NLVPLPEAL 298.
DB 245 NLDEFPTAI 253

RESULT 4
LGR5_MOUSE
AC Q921P4; STANDARD; PRT; 907 AA.
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Leucine-rich repeat-containing G protein-coupled receptor 5 precursor
DE (G protein-coupled receptor 49) (Orphan G protein-coupled receptor
DE FE).
DE GPR49 OR LGR5 OR FE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=99121227; PubMed=9920770;
RA Herney G., Methner A., Schaller H.C., Hermans-Borgmeyer I.;
RT "Identification of a novel seven-transmembrane receptor with homology
RT to glycoprotein receptors and its expression in the adult and
RT developing mouse.";
RL Biochem. Biophys. Res. Commun. 254:273-279 (1999).
CC -!- FUNCTION: Orphan receptor. It may be an important receptor for
CC signals controlling growth and differentiation of specific

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CC embryonic tissues.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed in the gonads, the adrenal gland,
CC and in the brain. In the central nervous system expression is
CC restricted to the olfactory bulb. In the adrenal gland detected
CC only in the neural-crest derived chromaffin cells of the
CC medulla, but not in the cells of the adrenal cortex. In the
CC gonads, the expression is high in Graafian follicle, but absent
CC from primary and secondary follicles.
CC -!- DEVELOPMENTAL STAGE: Expressed from embryonic day 10.5 (E10.5) in
CC the developing spinal cord and in the neuroepithelia of the
CC myel-, met-, mes-, and diencephalon. Expression is transitory and
CC the pattern changed rapidly.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -!- SIMILARITY: Contains 17 leucine-rich (LRR) repeats.
CC
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CC
CC -----
CC EMBL; AF110818; AAD14684.1; -.
CC HSP; P23945; 1XUN.
CC MGD; MG1:1341817; Gpr49.
CC InterPro; IPR000276; GPCR_Rhodospn.
CC InterPro; IPR001611; LRR.
CC InterPro; IPR000372; LRR_Nterm.
CC InterPro; IPR003591; LRR_Typ.
CC Pfam; PF00001; 7tm_1; 1.
CC Pfam; PF00560; LRR; 14.
CC Pfam; PF01462; LRRNT; 1.
CC PRINTS; PR00237; GPCR_RHODOPSIN.
CC PRINTS; PR00019; LEURICHRPT.
CC SMART; SM00369; LRR_TYP; 8.
CC SMART; SM00013; LRRNT; 1.
CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; FALSE_NEG.
CC PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
CC G-protein coupled receptor; Signal; Transmembrane; Glycoprotein;
CC Repeat; Leucine-rich repeat.
CC SIGNAL 1 21 POTENTIAL.
CC CHAIN 22 907 LEUCINE-RICH REPEAT-CONTAINING G PROTEIN-
CC COUPLED RECEPTOR 5.
CC DOMAIN 22 561 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 562 582 1 (POTENTIAL).
CC DOMAIN 583 593 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 594 614 2 (POTENTIAL).
CC DOMAIN 615 638 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 639 659 3 (POTENTIAL).
CC DOMAIN 660 682 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 683 703 4 (POTENTIAL).
CC DOMAIN 704 723 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 724 744 5 (POTENTIAL).
CC DOMAIN 745 767 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 768 788 6 (POTENTIAL).
CC DOMAIN 789 802 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 803 823 7 (POTENTIAL).
CC DOMAIN 824 907 CYTOPLASMIC (POTENTIAL).
CC REPEAT 64 88 LRR 1.
CC REPEAT 89 112 LRR 2.
CC REPEAT 113 136 LRR 3.
CC REPEAT 137 160 LRR 4.
CC REPEAT 162 184 LRR 5.
CC REPEAT 186 208 LRR 6.
CC REPEAT 209 232 LRR 7.
CC REPEAT 233 256 LRR 8.
CC REPEAT 257 279 LRR 9.
CC REPEAT 281 303 LRR 10.
CC REPEAT 304 327 LRR 11.
CC REPEAT 328 350 LRR 12.
CC REPEAT 351 375 LRR 13.

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Qy 52 MPVPIPLDTAHLDSLNNRLEWNEVSLAGPGYTTLAGLDLHNLNLTSTPTAFSLRYLE 111
Db 51 VPEGLSAFTQALDISMNNITQLPED--AFKPPFLEELQAGNDLSFIHPKALSGLKELK 108
Qy 112 SLDSHNGLTALPAESTS--SPISDVNLSHNLQREVSVAFTHSQGRALHVDLSHNLH 170
Db 109 VLTQNNQLKTVFSEATRGSLQSLQSLDLNHNITSPEDSFEGVLQRL--HLWLDNSLT 166
Qy 171 RLVPHPTRAGLPAPTIOQLNLAHNLHVP-----NLRDPLRYLSLDGPNLAVIGPGAF 225
Db 167 EVVHPJUS--NLPTQALTLALNKISSIDPFAFNLSLWV--LHLHNNKIRGLSQHCF 221
Qy 226 AGLGLGLTHLSLA-----SLQRLPELAPSGFRE-----LPGQLVLDLSG 263
Db 222 DGLDNLETLDLSYNNLGEFFQAIKARPSLKELGFHNSISVIPDGAFGNPLRTIHL 281
Qy 264 NPKLNWAGAEVFSGLSS-----LQELDLSGTNLVLPPEAL-- 298
Db 282 NP--LSFVGNFAFNLSLHSLVIRGASMKVQFPNLTGTVHLESUTLTGKISSIPNLCQ 340
Qy 299 -----LLHLPALQSVSGQDVRCR-----LVREGTY-----PRPGSSPKVP 336
Db 341 EOKMLRTLDLSYNNIRDLPSFNGCHALEEISLQRNQIVQIKEGTFQGLISLRILDSRNL 400
Qy 337 LHCVDTRSAARGP 350
Db 401 IHEIHSRAFATLGP 414

RESULT 6
LGR4_RAT
ID LGR4_RAT STANDARD; PRT; 951 AA.
AC Q922H4;
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Leucine-rich repeat-containing G protein-coupled receptor 4 precursor.
GN GPR48 OR LGR4;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=99065210; PubMed=9849958;
RX Hsu S.Y., Liang S.-G., Hsueh A.J.W.;
RT "Characterization of two LGR genes homologous to gonadotropin and
RT thyrotropin receptors with extracellular leucine-rich repeats and a G
RL protein-coupled, seven-transmembrane region.";
RL Mol. Endocrinol. 12:1830-1845(1998).
CC -!- FUNCTION: Orphan receptor.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -!- SIMILARITY: Contains 15 leucine-rich (LRR) repeats.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: AF061443; AAC77910.1;
CC InterPro: IPR000276; GPCR_Rhodpsn.
CC InterPro: IPR001611; LRR.
CC InterPro: IPR000372; LRR_Nterm.
CC InterPro: IPR003591; LRR_Typ.
CC Pfam: PF00001; 7tm 1; 1.
CC Pfam: PF00560; LRR; 15.
CC Pfam: PF01462; LRRNT; 1.

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DR PRINTS; PR00237; GPCR_HODPSN.
DR PRINTS; PR00019; LEURICHRPT.
DR SMART; SM00369; LRR_TYP; 5.
DR SMART; SM00013; LRRNT; 1.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR F1_1; FALSE_NEG.
DR PROSITE; PS00262; G-PROTEIN RECEPTOR F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Signal; Glycoprotein;
KW Repeat; Leucine-rich repeat.
FT SIGNAL 1 24
FT CHAIN 25 951
FT DOMAIN 25 544
FT TRANSMEM 545 565
FT DOMAIN 566 575
FT TRANSMEM 576 586
FT DOMAIN 597 619
FT TRANSMEM 620 640
FT DOMAIN 641 661
FT TRANSMEM 662 682
FT DOMAIN 683 703
FT TRANSMEM 704 724
FT DOMAIN 725 756
FT TRANSMEM 757 777
FT DOMAIN 778 783
FT TRANSMEM 784 804
FT DOMAIN 805 951
FT REPEAT 55 79
FT REPEAT 81 103
FT REPEAT 104 127
FT REPEAT 128 151
FT REPEAT 153 175
FT REPEAT 176 199
FT REPEAT 200 223
FT REPEAT 225 247
FT REPEAT 248 270
FT REPEAT 272 294
FT REPEAT 318 341
FT REPEAT 342 366
FT REPEAT 368 387
FT REPEAT 388 411
FT REPEAT 413 435
FT REPEAT 436 463
FT DISULFID 618 693
FT CARBOHYD 68 68
FT CARBOHYD 188 188
FT CARBOHYD 199 199
FT CARBOHYD 294 294
FT CARBOHYD 314 314
FT CARBOHYD 505 505
SQ SEQUENCE 951 AA; 104138 MW; 5ED56AC072123461 CRC64;
Query Match 14.0%; Score 256; DB 1; Length 951;
Best Local Similarity 25.9%; Pred. No. 4.9e-11;
Matches 105; Conservative 51; Mismatches 149; Index 100; Gaps 14;
Qy 1 MPWPL-----LLLAVALSAQTRP--CFPGQCEVETFGLPDSFSLTRVDCSGLGPHI 51
Db 1 MPGLGLLCLFALGLGSGAGSAAAPLCAAPCSGDD-----RVDCSGKGLTA 50
Qy 52 MPVPIPLDTAHLDSLNNRLEWNEVSLAGPGYTTLAGLDLHNLNLTSTPTAFSLRYLE 111
Db 51 VPEGLSAFTQALDISMNNITQLPED--AFKPPFLEELQAGNDLSFIHPKALSGLKELK 108
Qy 112 SLDSHNGLTALPAESTS--SPISDVNLSHNLQREVSVAFTHSQGRALHVDLSHNLH 170
Db 109 VLTQNNQLKTVFSEATRGSLQSLQSLDLNHNITSPEDSFEGVLQRLHLD-----DN 163
Qy 171 RLVPHPTRAGLPAPTIOQLNLAHNLHVP-----NLRDPLRYLSLDGPNLAVIGPGAF 225
Db 164 SLTEVPVRLSNLPTLQALTLALNKISSIDPFAFNLSLWV--LHLHNNKIRGLSQHCF 221
Qy 226 AGLGLGLTHLSL-----ASLQRLPELAPSGFRE-----LPGQLVLDLSG 263
Db 222 DGLDNLETLDLSYNNLGEFFQAIKARPSLKELGFHNSISVIPDGAFGNPLRTIHL 281

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QY 264 NPKLNWAGAEVPSGLSS-----LQELDLSTNLVPLPEAL-- 298  
 DB 282 NP-LSFVGNASPHNLSDLHCLVIRGASLVQVFPNLTGTVHLESITLGTGKISSIPDDLQ 340  
 QY 299 -----LLHLPALQSVSGQDVRCR-----LVREGY 325  
 DB 341 NQKMLRTLDLSYNNIRDLPSFNGCFRALEISLQNOISLIKENTF 385

## RESULT 7

AZGL HUMAN  
 ID AZGL HUMAN STANDARD; PRT; 347 AA.  
 AC P02750; Q96Q24;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Leucine-rich alpha-2-glycoprotein precursor (LRG).  
 GN LRG.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA O'Donnell L.C., Druhan L.J., Avalos B.R.;  
 RT "Molecular characterization and expression analysis of leucine-rich  
 RT alpha-2-glycoprotein, a novel marker of granulocytic  
 RT differentiation."  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE OF 36-347.  
 RX MEDLINE=85166241; PubMed=3856868;  
 RA Takahashi N., Takahashi Y., Putnam F.W.;  
 RT "Periodicity of leucine and tandem repetition of a 24-amino acid  
 RT segment in the primary structure of leucine-rich alpha 2-glycoprotein  
 RT of human serum."  
 RL Proc. Natl. Acad. Sci. U.S.A. 82:1906-1910(1985).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Plasma.  
 CC -!- SIMILARITY: Contains 8 leucine-rich (LRR) repeats.  
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 DR EMBL; AF403428; AAK95527.1; -  
 DR SWISS-2DPAGE; P02750; HUMAN.  
 DR Sienna-2DPAGE; P02750; -  
 DR GO; GO:0016020; C:membrane; NAS.  
 DR InterPro; IPR001611; LRR.  
 DR InterPro; IPR000483; LRR\_Cterm.  
 DR InterPro; IPR003591; LRR\_typ.  
 DR Pfam; PF00560; LRR; 8.  
 DR Pfam; PF01463; LRRCT; 1.  
 DR PRINTS; PR00019; LEURICHRPT.  
 DR SMART; SM00369; LRR\_TYP; 4.  
 DR SMART; SM00082; LRRCT; 1.  
 KW Plasma; Glycoprotein; Repeat; Leucine-rich repeat; Signal.  
 FT SIGNAL 1 35  
 FT CHAIN 36 347 LEUCINE-RICH ALPHA-2-GLYCOPROTEIN.  
 FT REPEAT 91 114 LRR 1.  
 FT REPEAT 115 138 LRR 2.  
 FT REPEAT 140 162 LRR 3.  
 FT REPEAT 163 186 LRR 4.  
 FT REPEAT 188 210 LRR 5.  
 FT REPEAT 212 234 LRR 6.  
 FT REPEAT 235 258 LRR 7.  
 FT REPEAT 259 282 LRR 8.

FT DISULFID 43 56  
 FT DISULFID 303 329  
 FT CARBOHYD 37 37  
 FT CARBOHYD 79 79  
 FT CARBOHYD 186 186  
 FT CARBOHYD 269 269  
 FT CARBOHYD 325 325  
 FT CARBOHYD 306 306  
 SQ SEQUENCE 347 AA; 38178 MW; 20C99ED50152FA9C CRC64;  
 Query Match 13.6%; Score 248; DB 1; Length 347;  
 Best Local Similarity 33.0%; Pred. No. 5.2e-11;  
 Matches 106; Conservative 34; Mismatches 117; Indels 64; Gaps 16;  
 QY 5 LLLLLAVSG-AQTRPCFCQCEVETFGLPDSFSLTRVDCSGLGPHIMPVPIPLDTAHL 63  
 DB 25 LLLLLAASAWGVTLSF--KDCQ-----VFPSDHGSSISCO--PFAEIPGYLPADTVHL 73  
 QY 64 DLSSNLEMNESVLAPGYTTIAGLDLHSHNLTISPTAFSRRLRYLSLDLHSHNLTAL 123  
 DB 74 AVEFFNLTHLPANLLQGA--SKQLHLHSSNGLESLSPEFLPVPQLAVLDLTRNALTGL 131  
 QY 124 PAESF--TSSPLSDVNLHNLREVSVAFTTHSQGRALHVDLHSHNLIHRLVPHPTAGLP 182  
 DB 132 PFGLFQASATLDTLVLENQLEVLVS--WLHGLKALGHLDLSGNRLKLP-----GUL 184  
 QY 183 A--PTIQSLNLANRHLHVPN--LR-DLPLRYLSLDGNPLAVIGPAGAGLGLTHLSLA 237  
 DB 185 ANFTLRTLDLGENQLETPDLLRGPLQLERLHLEGNKLVLGKDLL----- 232  
 QY 238 SLQRLPELAPSGFRELPGIQLVLDLSGNPKLNWAGAEVPSGLSSLQELDLSTNLVPLPEA 297  
 DB 233 ----LPQ-----PDLYLFLNGN-KLARVAAGAFQGLRQDLMDLSNNSLASVPEG 278  
 QY 298 LLLHLPALQSVSGQ---DVR 315  
 DB 279 LW-----ASLGQPNWDMR 291  
 RESULT 8  
 GPV HUMAN  
 ID GPV HUMAN STANDARD; PRT; 560 AA.  
 AC P40197;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Platelet glycoprotein V precursor (GPV) (CD42D).  
 GN GP5.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lung;  
 RX MEDLINE=93391348; PubMed=7690959;  
 RA Hickey M.J., Hagen F.S., Yagi M., Roth G.J.;  
 RT "Human platelet glycoprotein V: characterization of the polypeptide  
 RT and the related Ib-V-IX receptor system of adhesive, leucine-rich  
 RT glycoproteins."  
 RL Proc. Natl. Acad. Sci. U.S.A. 90:8327-8331(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Platelet;  
 RX MEDLINE=94012616; PubMed=8407908;  
 RA Lanza F., Morales M., de la Salle C., Cazenave J.-P., Clemençon K.J.,  
 RA Shimomura T., Phillips D.R.;  
 RT "Cloning and characterization of the gene encoding the human platelet  
 RT glycoprotein V. A member of the leucine-rich glycoprotein family  
 RT cleaved during thrombin-induced platelet activation."  
 RL J. Biol. Chem. 268:20801-20807(1993).  
 RN [3]  
 RP PARTIAL SEQUENCE.